

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:49:56 ; Search time 39 Seconds

(without alignments)  
249.177 Million cell updates/sec

Title: US-10-678-588a-8

Perfect score: 459  
Sequence: 1 REODRYLPANISIRIMKAL.....FEDYIEPLKYLKXREXEG 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417.5	91.0	179	2 S22820	transcription fact
2	407.5	88.8	228	2 T45874	transcription fact
3	405.5	88.3	138	2 E84810	hypothetical prote
4	400.5	87.3	161	2 G71407	transcription fact
5	393.5	85.7	178	2 A84788	probable CCAAT-box
6	376.5	82.0	215	2 F84508	probable CCAAT-box
7	373.5	73.5	180	2 S24469	transcription fact
8	373.5	73.5	205	2 S22817	transcription fact
9	373.5	73.5	207	2 F38245	transcription fact
10	337.5	73.5	207	2 A23692	transcription fact
11	336.5	72.0	186	2 JC6080	transcription fact
12	330.5	72.0	209	2 S22818	transcription fact
13	325.5	70.9	160	2 G84919	transcription fact
14	308.5	67.2	208	2 G86352	protein T26P17.20
15	288.5	62.9	144	1 A28123	transcription fact
16	280.5	61.1	139	2 C86222	hypothetical prote
17	280.5	61.1	205	2 S51565	transcription fact
18	271.5	59.2	116	2 S42744	transcription fact
19	255.5	55.7	403	2 E88021	protein M10D9.4 [1
20	230	50.1	122	2 S22819	transcription fact
21	144.5	31.5	159	2 T50504	DR1-like protein -
22	142.5	31.0	159	2 S53582	TATA-binding prote
23	137	29.8	175	2 JC5365	TBP-binding repres
24	136	29.6	176	2 A43320	TBP-binding prote
25	119	25.9	161	2 T40194	probable transcrip
26	117	25.5	275	2 C84673	hypothetical prote
27	94.5	20.6	184	2 T22529	hypothetical prote
28	85.5	18.6	210	2 T40369	probable dna bindi
29	79.5	17.3	72	2 A69292	archaeal histone A

30	74.5	16.2	69	2 A35959	archaeal histone H
31	74.5	16.2	146	2 S69594	hypothetical prote
32	74	16.1	137	2 T34387	hypothetical prote
33	72.5	15.8	67	2 A64321	archaeal histone -
34	72.5	15.8	67	2 D64416	archaeal histone -
35	71.5	15.6	69	2 A47036	histone-related pr
36	71.5	15.6	69	2 T48848	histone Hmf1 limpo
37	70.5	15.4	752	2 A98111	maltoedextrin phosp
38	70.5	15.4	752	2 D95246	glycogen phosphory
39	69	15.0	2178	2 S29237	calcium channel pr
40	69	15.0	2222	2 A37490	calcium channel pr
41	69	15.0	2251	2 B54972	voltage-dependent
42	69	15.0	2259	2 S29236	voltage-dependent
43	69	15.0	2270	2 A54972	calcium channel pr
44	69	15.0	2272	2 C54972	voltage-dependent
45	68.5	14.9	697	2 F84646	hypothetical prote

#### ALIGNMENTS

```
RESULT 1
S22820
transcription factor NF-Y, CCAAT-binding, chain B - maize
N:Alternate names: CCAAT-box DNA-binding protein
C:Species: Zea mays (maize)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C/Accession: S22820
R/LI, X.Y.; Mantovan, R.; Van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Mathis, D.
Nucleic Acids Res. 20, 1087-1091, 1992
A:Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.
A:Reference number: S22816; MUID:92195809; PMID:11549471
A/Accession: S22820
A:Molecule type: mRNA
A:Residues: 1-179 <LI>
A:Cross-references: UNIPROT:P25209; EMBL:X59714
C:Superfamily: transcription factor HAP3
C:Keywords: DNA binding; transcription factor regulation
F/30-119/Domain: DNA binding #status predicted <DNA>

Query Match      91.0%; Score 417.5; DB 2; Length 179;
Best Local Similarity 83.2%; Pred. No. 3,2e-47;
Matches 84; Conservative 2; Mismatches 8; Gaps 1;

QY      1 REODRYLPANISIRIMKALPNXGKXXXXXXIAKDAKXTXQCVSFFISFTSASXKC 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      30 REODRYLPANISIRIMKALPNXGKXXXXXXIAKDAKXTXQCVSFFISFTSASXKC 82
QY      61 QXERKRTINGDDLLMAMATGFEFDYIEPLKYLKXREXEG 101
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      83 QXERKRTINGDDLLMAMATGFEFDYIEPLKYLKXREXEG 123

RESULT 2
T45874
transcription factor NF-Y, CCAAT-binding-like protein - Arabidopsis thaliana
N:Alternate names: protein FAP12.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45874
R/Bloeker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23016
A/Accession: T45874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-228 <BL>
A:Cross-references: UNIPROT:Q9LFI3; EMBL:AL132966
A:Experimental source: cultivar Columbia; BAC clone FAP12
C:Genetics:
A:Map position: 3
A:Insertions: 75/2; 116/3; 120/3; 145/3; 164/3; 179/3; 213/1
A>Note: FAP12.40
```

Query Match 88.8%; Score 407.5; DB 2; Length 228;  
Best Local Similarity 80.2%; Pred. No. 8,6e-46;  
Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
DB 28 REODRFLPIANISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSASXKC 80

QY 61 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 101  
DB 81 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 121

RESULT 3  
B84810  
hypothetical protein At2g38880 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: B84810  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: B84810  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-138 <STO>  
A/Cross-references: UNIPROT:Q9SLG0; GB:AE002093; NID:G3928076; PIDN:AACT9602.1; GSPDB:GN  
C/Genetics:  
A/Gene: At2g38880  
A/Map position: 2  
C/Superfamily: transcription factor HAP3

Query Match 88.3%; Score 405.5; DB 2; Length 138;  
Best Local Similarity 80.0%; Pred. No. 9,1e-46;  
Matches 80; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
DB 20 REODRFLPIANISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSASXKC 72

QY 61 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 100  
DB 73 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 112

RESULT 4  
G71407  
transcription factor, CCAAT-binding, chain A - Arabidopsis thaliana  
N/Alternate names: protein DL3310W  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
A/Variety: Columbia  
C/Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
C/Accession: G71407  
R/Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
P.; Medler, H.; Medler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel  
avaraugh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998  
A/Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech  
erhoff, A.; Moore, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And  
C.; Chludzinski, N.  
A/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
A/Reference number: A71400; MUID:98121113; PMID:9461215  
A/Accession: G71407  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-161 <BEV>  
A/Cross-references: UNIPROT:O23310; GB:Z97336; NID:G2244788; PIDN:CAB10233.1; PID:G22448  
C/Genetics:  
A/Map position: 4COP9-4G3845

A/Note: DL3310W  
C/Superfamily: transcription factor HAP3  
C/Keywords: DNA binding; transcription regulation  
P/20-109/Domain: DNA binding #status predicted <DNA>

Query Match 87.3%; Score 400.5; DB 2; Length 161;  
Best Local Similarity 78.2%; Pred. No. 4,9e-45;  
Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
DB 20 REODRFLPIANISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSASXKC 72

QY 61 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 101  
DB 73 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 113

RESULT 5  
A84788  
probable CCAAT-box binding transcription factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: A84788  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: A84788  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-178 <STO>  
A/Cross-references: UNIPROT:Q9ZQC3; GB:AE002093; NID:G4371295; PIDN:AA018153.1; GSPDB:GN  
C/Genetics:  
A/Gene: At2g37060  
A/Map position: 2

Query Match 85.7%; Score 393.5; DB 2; Length 178;  
Best Local Similarity 78.0%; Pred. No. 4,5e-44;  
Matches 78; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
DB 29 REODRFLPIANISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISFITSASXKC 81

QY 61 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 100  
DB 82 QXERKRTINGDDLMMAMATIGFEDYIEPLKYLXXYREXG 121

RESULT 6  
F84508  
probable CCAAT-box binding transcription factor [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: F84508  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
Euse, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: F84508  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-215 <STO>  
A/Cross-references: UNIPROT:Q9SIT9; GB:AE002093; NID:G4558662; PIDN:AA022680.1; GSPDB:GN  
C/Genetics:  
A/Gene: At2g13570  
A/Map position: 2

```

Query Match          92.0%; Score 376.5; DB 2; Length 215;
Best Local Similarity 70.3%; Pred. No. 9,66-42;
Matches 71; Conservative 10; Mismatches 13; Indels 7; Gaps 1.

Oy 1 REODRYLPANISRIMKTLPNNGCKXXXXXXXXXIANDAKTKQECVSEFISPTTSEASKCC 60
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 35 KQDQFPLIANVGRIMKVLPGNGK-----ISDADAEYQECVSEFISPTTGEASDKC 87
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy 61 QXKRRKTNGDDLAMAMATLGFEDYIEPLKVLXXYYREXEG 101
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 88 QREKRTINGDDIIWAITTLGFEDEVVAPLKVLLCKRYDTGEG 128
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
S24469
transcription factor NF-Y, CAAT-binding, chain B - chicken
C|Species: Gallus gallus (chicken)
C|Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C|Accession: S24469
R|Benoliet, C.
submitted to the EMBL Data Library, January 1992
A|Reference number: S24469
A|Accession: S24469
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-180 <BEN>.
A|Cross-references: EMBL.X59713; NID:g63690; PIDN:CAA4223.1; PID:g63691
C|Superfamily: transcription factor HAP3
C|Keywords: DNA binding; transcription regulation
C|51-140/Domain: DNA binding #status predicted <DNA>

```

Query Match	Similarity	Score	DB 2	Length
Best Local	67.3%	Pred. No. 11e-36;		
Matches	66;	Conservative 12;	Mismatches 13;	Indels 7; Gaps 1.
Oy	1	REODRYLIANISRMKKALPYNQGXGXKXXXXX	IADAKXTQECVSEFISFTSEASKC	60
		:::     ::	:::     ::	
		:::     ::	:::     ::	
Db	51	REQDYLPIANAVARIMKNAIPQTGK-----	IADDAECCVQECVSEFISFTSEASRC	103
Oy	61	QXERKRTINGDDLWAMATLGFEDYIRPLKVLXXXXRE		98
		:::     ::	:::     ::	
Db	104	HOEKRRTINGEDLIPAMSTLGGVYVEBPLKYLQKFRRE		141

```

RESULT 8
S22817
transcription factor NF-Y, CCAAT-binding, chain B - human
N|Alternate names: CCAAT-box DNA-binding protein
C|Species: Homo sapiens (man)
C|Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C|Accession: S22817
R|Li, X.Y.; Matcovani, R.; van Huijsduijn, R.H.; Andre, I.; Benoist, C.; Machius, D
Nucleic Acids Res. 20, 1087-1091, 1992
A|Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.
A|Reference number: S22816; MUID:92195809; PMID:1549471
A|Accession: S22817
A|Molecule type: mRNA
A|Residues: 1-205 <LIX>
A|Cross-References: EMBL:X59710; NID:g35049; PIDN:CAA42230.1; PID:g35050
C|Superfamily: Transcription factor HAP3
C|Keywords: DNA binding; transcription regulation
/51-140/Domain: DNA binding #status predicted <DNA>

```

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Query Match Similarity      73.5%; Score 337.5; DB 2; Length 205;
Best local similarity      67.3%; Pred. NO. 12e-36;
Matches      66; Conservative 12; Mismatches 13; Indels 7; Gaps 1.

QY      1 REODRYLPIANISRIKMLPANGKXXXXXXXXIADAKTKXQECVSEFISPTTSASKC 60
          |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      51 REQDIYLPANVARIMKNAIPQTK-----IADAEKVCQECSEFISPTTSASRC 103
          |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 QXKKKTNGDDLLMAAATLGFEDYIEPLKTYLXXYRE 98
          |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 104 HØKRKTINGEDILFAMSTLGFDSYVEPLKLYLQKFRE 141

## RESULT 5

transcription factor NF- $\gamma$ , CCNAT-binding, chain B - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: F38245; S12045  
R:Li, X.Y.; Hooft van Hujsduldjen, R.; Mantovani, R.; Benoist, C.; Machls, D.  
J. Biol. Chem. 267, 8984-8990, 1992  
A:Title: Intron-exon organization of the NF- $\gamma$  gene. Tissue-specific splicing modifies a  
A:Reference number: A38245; MUID:92250488; PMID:1577736  
A:Accession: F38245  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-207 <L1a>  
A:Cross-references: UNIPROT:P22569; GB:M86215  
R:Hooft van Hujsduldjen, R.; Li, X.Y.; Black, D.; Matches, H.; Benoist, C.; Machls, D.  
EMBO J. 9, 3119-3127, 1990  
A:Title: Co-evolution from yeast to mouse: CDNA cloning of the two NF- $\gamma$  (CP-1/CBP) subun  
A:Reference number: S12044; MUID:91006004; PMID:1658608  
A:Accession: S12045  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-207 <HOO>  
A:Cross-references: GB:X55316; NID:953362; PIDN:CA9024.1; PID:953363  
C:Superfamily: transcription factor HAP3  
C:Keywords: alternative splicing; DNA binding; transcription regulation

Query Match 73.5%, Score 337.5; DB 2; Length 207;  
 Best Local Similarity 67.3%; Pred. 1.2e-36;  
 Matches 66; Conservative 12; Mismatches 13; Gaps 1

```

QY      1 RQDGRYPININISIKKALPDKNGKXXXXXXXXXKADACKTQOECVSEISFTSRASKC 60
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      53 RQDITYPINAVAIIMKAIPTQTK-----IADKADCEQOECVSEISFTSRASRC 105
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 QXERKTINGDDLIAMATLGFEDYIEPLKYLXXYRE 98
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      106 HQERKTINGEDILFAMSTLGFDSYVEPLKYLQKPRE 143
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

```

RESULT 10
A23692
C:transcription factor, CCAAT-binding, chain A1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C:Accession: A23692
R:Vuorio, T.; Maltý, S.N.; de Crombrughe, B.
J. Biol. Chem. 265, 22480-22486, 1990
A:Title: Purification and molecular cloning of the "A" chain of a rat heteromeric CCAAT-
A:Reference number: A23692; MUID:91093096; PMID:226139
A:Accession: A23692
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <VUO>
A:Cross-references: UNIPROT:P22569; GB:M55045; GB:J05701; NID:G203352; PTDN:AAA40887.1;
C:Superfamily: transcription factor HAP3
C:Keywords: alternative splicing; DNA binding; transcription regulation
;53-142/Domain: DNA binding #status predicted <DNA>

```

```

Query Match 5.1; Score 337.5; DB 2; length 207;
Best Local Similarity 67.3%; Pred. No. 1,2e-36;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1

QY 1 REGRRYLPANISIRMKALPUNGQXXXXXXXXXADAKTQECVSEPISTPSRASKXC 60
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 53 REQDIYLPANVAKIMKALPQYGR-----IADADCEQVCEVSEPISTPSRASERC 105
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

QY 61 QXERKTINGDGLIMAMATLGPEDYIEPLKYLYLXXYYR 98
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DB 106 HQRRKTINGEDILFAMSTLGFDSVIEPLKYLYLQFRR 143
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

```

## RESULT 11

transcription factor HAP3 - *Emeticella nidulans*  
C/Species: *Emeticella nidulans*, *Aspergillus nidulans*  
C/Date: 21-Jan-1997 #sequence\_revision 21-Jan-1997 #text\_change 09-Jul-2004  
C/Accession: J06080  
R/Paragianopoulos, P.; Andrianopoulos, A.; Sharp, J.A.; Davis, M.A.; Hynes, M.J.  
Mol. Gen. Genet. 251, 412-421, 1996  
A/Title: The hapC gene of *Aspergillus nidulans* is involved in the expression of CCAAT-cc  
A/Reference number: J06080; MUID:96285564; PMID:8709944  
A/Accession: J06080  
A/Molecule type: mRNA  
A/Residues: 1-186 <PAP>  
A/Cross-references: UNIPROT:Q00735; GB:U5341; NID:g1017715; PIDN:AAC49411.1; PID:g10177  
C/Genetics:  
A/Genes: hapC  
A/Map position: 2  
A/Intons: 53/1; 90/1; 132/3  
C/Superfamily: transcription factor HAP3  
F/42-131/Domain: DNA binding #status predicted <DNA>

Query Match 73.3%; Score 336.5; DB 2; Length 186;  
Best Local Similarity 66.0%; Pred. No. 1.5e-36;  
Matches 66; Conservative 13; Mismatches 14; Indels 7; Gaps 1;  
Qy 1 REODRYIPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQCVSEFISFITSBAAXKC 60  
Db 42 KEODRWLPINAVNIRIMKALPENAK-----INAKAKCQVCVSEFISFITSBAEK 94  
Qy 61 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREX 100  
Db 95 QXERKTINGDDILFAMSTLGFEDYIEPLKYLXXYREX 134

## RESULT 12

transcription factor NF-Y, CCAAT-binding, chain B - see lamprey  
N/Alternate names: CCAAT-box DNA-binding protein  
C/Species: *Petromyzon marinus* (sea lamprey)  
C/Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 09-Jul-2004  
C/Accession: S22818; S78116  
R/Il, X.Y.; Mantovan, R.; van Huijsduijnen, R.H.; Andre, I.; Benoist, C.; Machie, D.  
Nucleic Acids Res. 20, 1087-1091, 1992  
A/Title: Evolutionary variation of the CCAAT-binding transcription factor NF-Y.  
A/Reference number: S22818; MUID:92195809; PMID:1549471  
A/Accession: S22818  
A/Molecule type: mRNA  
A/Residues: 1-209 <LIX>  
A/Cross-references: UNIPROT:P25210; EMBL:X59712  
R/Benoist, C.  
Submitted to the EMBL Data Library, January 1992  
A/Reference number: S78116  
A/Accession: S78116  
A/Molecule type: mRNA  
A/Residues: 1-110, 'R', 112-209 <BEN>  
A/Cross-references: EMBL:X55712; NID:964217; PIDN:CAA42232.1; PID:964218  
C/Superfamily: transcription factor HAP3  
C/Keywords: DNA binding; transcription regulation  
F/54-143/Domain: DNA binding #status predicted <DNA>

Query Match 72.0%; Score 330.5; DB 2; Length 209;  
Best Local Similarity 66.3%; Pred. No. 1e-35;  
Matches 65; Conservative 12; Mismatches 14; Indels 7; Gaps 1;  
Qy 1 REODRYIPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQCVSEFISFITSBAAXKC 60  
Db 54 REODIYIPINAVNIRIMKTSISGK-----IAKDAKCTQVCVSEFISFITSBAEBC 106  
Qy 61 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREX 98  
Db 107 HQEKKTINGDDILFAMSTLGFEDYIEPLKYLXXYREX 144

## RESULT 13

probable CCAAT-box binding transcription factor [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: G84919  
R/Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Mofat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;  
eues, D.; Nierman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: G84919  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-160 <STO>  
A/Cross-references: UNIPROT:O82248; GB:AE02093; NID:g3738293; PIDN:AAC63635.1; GSPDB:GN  
C/Genetics:  
A/Genes: At2g47810  
A/Map position: 2  
C/Superfamily: transcription factor HAP3

Query Match 70.9%; Score 325.5; DB 2; Length 160;  
Best Local Similarity 62.4%; Pred. No. 3.5e-35;  
Matches 63; Conservative 9; Mismatches 22; Indels 7; Gaps 1;  
Qy 1 REODRYIPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQCVSEFISFITSBAAXKC 60  
Db 50 KEODRLIPINAVNIRIMKNIIPANAK-----VSKAKETMORCVSEFISFIVGEASDKC 102  
Qy 61 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREX 101  
Db 103 HQERKTINGDDICWAPANLGFDDYIAQLKCYLHRYRVLE 143

## RESULT 14

protein T26F17.20 [imported] - *Arabidopsis thaliana*  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C/Accession: G86352  
R/Theologides, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hutzar, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Klm, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: G86352  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-208 <STO>  
A/Cross-references: UNIPROT:Q9SF08; GB:AE005172; NID:96552738; PIDN:AAFL6537.1; GSPDB:GN  
C/Genetics:  
A/Genes: T26F17.20  
A/Map position: 1

Query Match 67.2%; Score 308.5; DB 2; Length 208;  
Best Local Similarity 56.0%; Pred. No. 8e-33;  
Matches 56; Conservative 20; Mismatches 17; Indels 7; Gaps 1;  
Qy 1 REODRYIPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQCVSEFISFITSBAAXKC 60  
Db 28 REODIYIPINAVNIRIMKTPSHAK-----ISDAKETIQVCVSEFISFIVGEANBRC 80  
Qy 61 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREX 100



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:49:05 ; Search time 164 Seconds  
(without alignments)  
238.188 Million cell updates/sec

Title: US-10-678-588a-8  
Perfect score: 459  
Sequence: 1 REDDRFLPLANISIRIMKAL.....FEDYIEPLKYLXXYREXEG 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423.5	92.3	160	AD142339	AD142339 Plant tra
2	423.5	92.3	160	AD161959	AD161959 Plant pol
3	423.5	92.3	173	AD063706	AD063706 Transcript
4	423.5	92.3	173	AD161957	AD161957 Plant pol
5	423.5	92.3	174	AD063718	AD063718 Transcript
6	423.5	92.3	174	AD063704	AD063704 Transcript
7	423.5	92.3	174	AD161958	AD161958 Plant pol
8	417.5	91.0	178	ABG70264	ABG70264 LEC-1-rel
9	417.5	91.0	178	ABR40821	ABR40821 Zea mays
10	417.5	91.0	178	AD142322	AD142322 Plant tra
11	417.5	91.0	179	AD142323	AD142323 Plant tra
12	417.5	91.0	290	ADCC3665	ADCC3665 Polypepti
13	414.5	90.3	141	3 AAG04651	AAG04651 Arabidops
14	414.5	90.3	141	7 ADB37175	ADB37175 Plant yle
15	414.5	90.3	141	7 ADF50740	ADF50740 Thale cre
16	414.5	90.3	141	8 AD141625	AD141625 Plant tra
17	414.5	90.3	141	8 AD003369	AD003369 Thalecres
18	414.5	90.3	141	8 AD063929	AD063929 Transcript
19	414.5	90.3	141	8 AD161960	AD161960 Plant pol
20	414.5	90.3	182	ABG70259	ABG70259 LEC-1-rel
21	414.5	90.3	182	ABR40742	ABR40742 Triticum
22	413.5	90.1	177	5 ABG70249	ABG70249 LEC-1-rel
23	413.5	90.1	177	6 ABR40732	ABR40732 Eucalyptu
24	413.5	90.1	177	7 ADC23649	ADC23649 Polypepti
25	412.5	89.9	215	8 AD142328	AD142328 Plant tra

26	409.5	89.2	174	5	ABG70248	ABG70248 LEC-1-rel
27	409.5	89.2	174	6	ABR40731	ABR40731 Momordica
28	409.5	89.2	174	7	ADC23647	ADC23647 Polypepti
29	407.5	88.8	162	5	ABG70256	ABG70256 Polypepti
30	407.5	88.8	162	6	ABR40739	ABR40739 Glycine m
31	407.5	88.8	162	7	ADC23663	ADC23663 Polypepti
32	407.5	88.8	185	8	AD142329	AD142329 Plant tra
33	407.5	88.8	185	8	AD063668	AD063668 Transcript
34	407.5	88.8	185	8	AD161965	AD161965 Plant pol
35	407.5	88.8	228	5	ABG70263	ABG70263 LEC-1-rel
36	407.5	88.8	228	6	ABR40826	ABR40826 Arabidops
37	407.5	88.8	228	7	ADCC3666	ADCC3666 Polypepti
38	407.5	88.8	228	8	AD143709	AD143709 Plant tra
39	407.5	88.8	228	8	AD003497	AD003497 Thalecres
40	407.5	88.8	228	8	AD063035	AD063035 Transcript
41	407.5	88.8	228	8	AD161962	AD161962 Plant pol
42	407.5	88.8	228	8	AD161962	AD161962 Plant pol
43	406.5	88.6	164	5	ABG70250	ABG70250 LEC-1-rel
44	406.5	88.6	164	6	ABR40733	ABR40733 Zea mays
45	406.5	88.6	164	7	ADC23651	ADC23651 Polypepti

## ALIGNMENTS

RESULT 1	AD142339	standard; protein; 160 AA.
ID	AD142339	
XX	AD142339	
AC	AD142339	
XX	22-APR-2004	(first entry)
DT	22-APR-2004	(first entry)
XX		
DE	Plant transcription factor #319.	
XX		
KW	transgenic; plant; enhanced tolerance to abiotic stress;	
KW	glycosphoric tolerance; hormone sensitivity; disease resistance;	
KW	sugar sensing; flowering; flower structure; stem bifurcation;	
KW	branching pattern; apical dominance; trichome; stem morphology;	
KW	root growth; root hair; seed development; cell proliferation;	
KW	cell differentiation; premature senescence; necrosis; plant size;	
KW	leaf morphology; seed morphology; seed biochemistry; root anthocyanin;	
KW	plant anthocyanin; light response; shade avoidance; bioinformatic;	
KW	transcription factor; gene; ds.	
XX		
OS	Glycine max.	
XX		
PN	US2004019927-A1.	
XX		
PD	29-JAN-2004.	
XX		
PF	25-FEB-2003; 2003US-00374780.	
XX		
PR	18-APR-2001; 2001US-00637944.	
XX		
PA	(SHER/) SHERMAN B K.	
PA	(RIEC/) RIECHMANN J L.	
PA	(JIAN/) JIANG C.	
PA	(HEAR/) HEARD J E.	
PA	(HAAR/) HAAKE V.	
PA	(CREE/) CREELMAN R A.	
PA	(RATC/) RATCLIFFE O.	
PA	(ADAM/) ADAM L J.	
PA	(REUB/) REUBER T L.	
PA	(KEDD/) KEDDIE J.	
PA	(BROU/) BROUN P E.	
PA	(PIIG/) PILGRIM M L.	
PA	(DUBE/) DUBELA A N.	
PA	(PINE/) PINEDA O.	
XX	(YUGG/) YU G.	
PI	Sherman BK, Riechmann J, Jiang C, Heard J, Haake V, Creeleman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,	

PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
 XX WPI; 2004-132245/13.  
 XX  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX  
 PS Claim 1; SEQ ID NO 802; 435pp; English.  
 XX  
 CC The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glyphosate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure; change in stem bifurcations; altered branching  
 CC pattern; reduced apical dominance; reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins; or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor, and an orthologue of Arabidopsis thaliana  
 CC transcription factors isolated in the invention, that can be used in the  
 CC creation of a transgenic plant with altered traits.  
 CC  
 SQ Sequence 160 AA;  
 XX  
 Query Match 92.3%; Score 423.5; DB 8; Length 160;  
 Best Local Similarity 85.1%; Pred. No. 2.2e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPIANISIRIMKALPXNGKXXXXXXXXXIAKDAKTXQCVSEFISFISSEASXKC 60  
 DB 27 REODRYLPIANISIRIMKALPPNGK-----IAKDAKTMQCVSEFISFISSEASXKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFSDYIEPLKVLXYXREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFSDYIEPLKVLXYXREXEG 120  
 RESULT 2  
 ADS16959 standard; protein; 160 AA.  
 XX  
 AC ADS16959;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Plant polypeptide #18.  
 XX  
 KM Abiotic stress tolerance; LIL-related CCAAT transcription factor;  
 KM B domain; heat tolerance; drought stress tolerance; cold tolerance;  
 KM salt stress tolerance; MYB-related transcription factor;  
 KM seedling germination.  
 XX  
 OS Undefined.  
 XX  
 PN WO2004076638-A2.  
 XX  
 PD 10-SEP-2004.  
 XX  
 PF 25-FEB-2004; 2004WO-US005654.  
 XX  
 PR 25-FEB-2003; 2003US-00374780.  
 PR 30-SEP-2003; 2003US-00675852.  
 XX

PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Sherman BK, Riechmann UL, Ratcliffe O, Jiang C, Heard JE;  
 PI Haake V, Creelman RA, Adam LJ, Reuber LT, Keddle JS, Dubell AN;  
 PI Pineda O, Repetti PP, Century KS, Guterson NI, Yu G, Brown PE;  
 PI Kimimoto RW, Pilgrim ML;  
 XX WPI; 2004-653405/63.  
 DR  
 XX  
 PT New transgenic plant having increased abiotic stress tolerance as  
 PT compared to non-transgenic plants of the same species, useful in  
 PT bioinformatic research methods.  
 XX  
 PS Disclosure; Fig 10; 297pp; English.  
 XX  
 CC The invention relates to a transgenic plant having increased abiotic  
 CC stress tolerance as compared to non-transgenic plants of the same  
 CC species, where the transgenic plant comprises in its genome a transgene  
 CC encoding a polypeptide member of the G482 subclade of the non-LBCL-like  
 CC clade of proteins of the LIL-related CCAAT transcription factor family,  
 CC where overexpression of the polypeptide member confers abiotic stress  
 CC tolerance. The invention also relates to a seed from the transgenic  
 CC plant, a method for producing a transgenic plant having increased  
 CC tolerance to abiotic stress comprising providing an expression vector  
 CC comprising the polynucleotide sequence encoding the polypeptide, and  
 CC regulatory elements operably linked to the nucleotide sequence, where the  
 CC regulatory elements are effective to control expression of the nucleotide  
 CC sequence in a target plant, introducing the expression vector into a  
 CC plant cell, growing the plant cell, allowing the plant to overexpress the  
 CC polypeptide and identifying the one or more abiotic stress tolerant plants so  
 CC produced by comparing the one or more abiotic stress tolerant plants with  
 CC one or more non-transgenic plants of the same species, and a method for  
 CC increasing a plant's tolerance to abiotic stress comprising providing the  
 CC vector cited above and transforming the target plant with the vector to  
 CC generate a transformed plant with increased tolerance to abiotic stress,  
 CC compared to non-transgenic plants of the same species. The transgenic  
 CC plant comprises a polypeptide comprising a B domain. The B domain binds  
 CC to DNA at a transcription-regulating region comprising the motif CCAAT,  
 CC where the binding regulates transcription of the DNA. The regulation of  
 CC transcription confers increased abiotic stress tolerance in the  
 CC transgenic plant as compared to non-transgenic plants of the same  
 CC species. The abiotic stress tolerance is selected from heat tolerance,  
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The  
 CC transgenic plant further comprises a constitutive, inducible, or tissue-  
 CC specific promoter operably linked to the recombinant polynucleotide. The  
 CC recombinant polynucleotide is incorporated into an expression vector  
 CC comprising one or more regulatory elements that are effective to control  
 CC expression of the recombinant polynucleotide in a target plant. The  
 CC transgenic plant is a cultured host cell. The transgenic plant can  
 CC comprise in its genome a transgene encoding a polypeptide member of the  
 CC MYB-related transcription factor family, where overexpression of the  
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant  
 CC is useful in bioinformatic research methods. The invention provides  
 CC transgenic plants with improved seedling germination and performance  
 CC under conditions of limited nitrogen. This sequence represents a  
 CC polypeptide used in the scope of the invention.  
 CC  
 SQ Sequence 160 AA;  
 XX  
 Query Match 92.3%; Score 423.5; DB 8; Length 160;  
 Best Local Similarity 85.1%; Pred. No. 2.2e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPIANISIRIMKALPXNGKXXXXXXXXXIAKDAKTXQCVSEFISFISSEASXKC 60  
 DB 27 REODRYLPIANISIRIMKALPPNGK-----IAKDAKTMQCVSEFISFISSEASXKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFSDYIEPLKVLXYXREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFSDYIEPLKVLXYXREXEG 120  
 RESULT 3

AD063706  
 ID AD063706 standard; protein: 173 AA.  
 XX  
 AC AD063706;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Transcription factor G3471 orthologous sequence, SEQ ID 2173.  
 XX  
 XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 KM osmotic stress tolerance; cold tolerance; heat tolerance;  
 KM low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KM glyphosate resistance; flowering; fertility; seed development.  
 XX  
 OS Glycine max.  
 XX  
 PN MO2004031349-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 18-SEP-2003; 2003MO-US030292.  
 XX  
 PR 18-SEP-2002; 2002US-0411837P.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 24-APR-2003; 2003US-0465809P.  
 XX  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Jiang C, Heard JB, Ratcliffe O, Creelman RA, Adam LJ, Reuber TJ;  
 PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK,  
 PI WPI; 2004-330163/30.  
 XX  
 DR N-PSDB; AD063705.  
 XX  
 PT New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.  
 XX  
 PS Disclosure, SEQ ID NO 2173; 510pp; English.

CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 173 AA;  
 XX  
 QY Query Match 92.3%; Score 423.5; DB 8; Length 173;  
 Db Best Local Similarity 85.1%; Pred. No. 2,5e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPTANISRIKKALPXNGKXXXXXXIAKDAKTXQCVSEFISFISBA5XKC 60  
 Db 26 REODRYLPTANISRIKKALPXNGK-----IAKDAKTXQCVSEFISFISBA5XKC 78  
 QY 61 QXERKTINGDDLLMAMATLGFEDYTEPLKLYLXXYREXEG 101  
 Db 79 QXERKTINGDDLLMAMATLGFEDYTEPLKLYLARBREAEG 119  
 XX  
 RESULT 4  
 AD063706 standard; protein: 173 AA.  
 XX  
 AC AD063706;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Plant polypeptide #16.  
 XX  
 KM Abiotic stress tolerance; LIL-related CCAT transcription factor;  
 KM B domain; heat tolerance; drought stress tolerance; cold tolerance;  
 KM salt stress tolerance; MYB-related transcription factor;  
 KM seedling germination.  
 XX  
 OS Undentified.  
 XX  
 PN MO2004076638-A2.  
 XX  
 PD 10-SEP-2004.  
 XX  
 PF 25-FEB-2004; 2004MO-US005654.  
 XX  
 PR 25-FEB-2003; 2003US-00374780.  
 PR 30-SEP-2003; 2003US-00675852.  
 XX  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Sherman BK, Riechmann JL, Ratcliffe O, Jiang C, Heard JB;  
 PI Haake V, Creelman RA, Adam LJ, Reuber TJ, Keddie JS, Dubell AN;  
 PI Plameda O, Repetti PP, Century KS, Guttersen NI, Yu G, Brown PE;  
 PI Kimimoto RW, Pilgrim ML;  
 XX  
 DR WPI; 2004-653405/63.  
 XX  
 PT New transgenic plant having increased abiotic stress tolerance as  
 PT compared to non-transgenic plants of the same species, useful in  
 PT bioinformatic research methods.  
 XX  
 PS Disclosure, Fig 10; 297pp; English.

CC sequence in a target plant, introducing the expression vector into a  
 CC plant cell, growing the plant cell, allowing the plant to overexpress the  
 CC polypeptide and identifying one or more abiotic stress tolerant plants so  
 CC produced by comparing the one or more abiotic stress tolerant plants with  
 CC one or more non-transgenic plants of the same species, and a method for  
 CC increasing a plant's tolerance to abiotic stress comprising providing the  
 CC vector cited above and transforming the target plant with the vector to  
 CC generate a transformed plant with increased tolerance to abiotic stress,  
 CC compared to non-transgenic plants of the same species. The transgenic  
 CC plant comprises a polypeptide comprising a B domain. The B domain binds  
 CC to DNA at a transcription-regulating region comprising the motif CCAAT,  
 CC where the binding regulates transcription of the DNA. The regulation of  
 CC transcription confers increased abiotic stress tolerance in the  
 CC transgenic plant as compared to non-transgenic plants of the same  
 CC species. The abiotic stress tolerance is selected from heat tolerance,  
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The  
 CC transgenic plant further comprises a constitutive, inducible, or tissue-  
 CC specific promoter operably linked to the recombinant polynucleotide. The  
 CC recombinant polynucleotide is incorporated into an expression vector  
 CC comprising one or more regulatory elements that are effective to control  
 CC expression of the recombinant polynucleotide in a target plant. The  
 CC transgenic plant is a cultured host cell. The transgenic plant can  
 CC comprise in its genome a transgene encoding a polypeptide member of the  
 CC MYB-related transcription factor family, where overexpression of the  
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant  
 CC is useful in bioinformatic research methods. The invention provides  
 CC transgenic plants with improved seedling germination and performance  
 CC under conditions of limited nitrogen. This sequence represents a  
 CC polypeptide used in the scope of the invention.

CC Sequence 173 AA;

CC Query Match 92.3%; Score 423.5; DB 8; Length 173;  
 CC Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 CC Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

CC QY 1 REODRYLPIANISRIKMKALPXNGKXXXXXXIAKDAKXTXOCVSEFISFITSASXKC 60  
 CC DB 26 REODRYLPIANISRIKMKALPPNGK-----IAKDAKXTXOCVSEFISFITSASXKC 78  
 CC QY 61 QXERKRTINGDDLLMMATGFFEDYIEPLKVTLYXXYREXEG 101  
 CC DB 79 QXERKRTINGDDLLMMATGFFEDYIEPLKVTLYARREXEG 119

CC RESULT 5

CC ID ADO63718 standard; protein; 174 AA.

CC AC ADO63718;

CC DT 15-JUL-2004 (first entry)

CC XX Transcription factor G3477 orthologous sequence, SEQ ID 2185.

CC XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;

CC KM osmotic stress tolerance; cold tolerance; heat tolerance;

CC KM low nitrogen tolerance; low phosphate tolerance; fungal disease;

CC KM glycosylate resistance; flowering; fertility; seed development.

CC OS glycine max.

CC XX WO2004031349-A2.

CC PN 15-APR-2004.

CC XX 18-SEP-2003; 2003WO-US030292.

CC XX 18-SEP-2002; 2002US-0411837P.

CC PR 17-DEC-2002; 2002US-0434166P.

CC PR 24-APR-2003; 2003US-0465809P.

CC XX (MENDEL) MENDEL BIOTECHNOLOGY INC.

XX Jiang C, Heard JF, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL,  
 CC PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK,  
 CC DR WPI; 2004-330163/30.  
 CC PT N-PSDB; ADO63717.  
 CC PT New recombinant polynucleotide encoding transcription factor  
 CC PT polypeptides, useful for producing transgenic plants with advantageous  
 CC properties compared to a reference plant.

CC PS Disclosure; SEQ ID NO 2185; 510pp; English.

CC The present invention relates to novel plant transcription factor  
 CC proteins (i) and nucleotide sequences (ii) (ADO61534-ADO63718). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (ii), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stress,  
 CC increased tolerance to osmotic stress, increased tolerance to cold,  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly Erysiphe, Fusarium and Botrytis,  
 CC increased tolerance to multiple fungal pathogens, increased resistance to  
 CC glycosylate, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced  
 CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC avoidance, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprotein content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
 CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC CC ftp.wipo.int/pub/published\_pct\_sequences.

CC SQ Sequence 174 AA;

CC Query Match 92.3%; Score 423.5; DB 8; Length 174;  
 CC Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 CC Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

CC QY 1 REODRYLPIANISRIKMKALPXNGKXXXXXXIAKDAKXTXOCVSEFISFITSASXKC 60  
 CC DB 27 REODRYLPIANISRIKMKALPPNGK-----IAKDAKXTXOCVSEFISFITSASXKC 79  
 CC QY 61 QXERKRTINGDDLLMMATGFFEDYIEPLKVTLYXXYREXEG 101  
 CC DB 80 QXERKRTINGDDLLMMATGFFEDYIEPLKVTLYARREXEG 120

CC RESULT 6

CC ID ADO63704 standard; protein; 174 AA.

CC AC ADO63704;

CC DT 15-JUL-2004 (first entry)

XX Transcription factor G3470 orthologous sequence, SEQ ID 2171.  
 DE Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
 XX osmotic stress tolerance; cold tolerance; heat tolerance;  
 KM low nitrogen tolerance; low phosphate tolerance; fungal disease;  
 KM glyphosate resistance; flowering; fertility; seed development.  
 XX  
 OS Glycine max.  
 PN WO2004031349-A2.  
 PD 15-APR-2004.  
 XX 18-SEP-2003; 2003WO-US030292.  
 PF 18-SEP-2002; 2002US-0411837P.  
 PR 17-DEC-2002; 2002US-0434166P.  
 PR 24-APR-2003; 2003US-0465809P.  
 XX  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 PI Jiang C, Heard JR, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;  
 PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK,  
 DR WPI; 2004-330163/30.  
 XX N-PSDB; ADO63703.  
 PT New recombinant polynucleotide encoding transcription factor  
 PT polypeptides, useful for producing transgenic plants with advantageous  
 PT properties compared to a reference plant.  
 PS Disclosure; SEQ ID NO 2171; 510bp; English.  
 XX  
 CC The present invention relates to novel plant transcription factor  
 CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The  
 CC sequences can be used to produce transgenic plants, which overexpress  
 CC (II), where the transgenic plant has an altered trait as compared to a  
 CC non-transgenic plant or wild-type plant. The transgenic plant comprises  
 CC an altered trait selected from increased tolerance to abiotic stresses,  
 CC increased tolerance to osmotic stress, increased tolerance to cold,  
 CC increased germination in cold, increased tolerance to heat, increased  
 CC germination in heat, increased tolerance to freezing conditions,  
 CC increased tolerance to low nitrogen conditions, increased tolerance to  
 CC low phosphate conditions, increased tolerance to disease, including  
 CC fungal disease and particularly *Erysiphe*, *Fusarium* and *Botrytis*,  
 CC increased tolerance to multiple fungal pathogens, increased resistance to  
 CC glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,  
 CC increased sensitivity to ACC, altered sugar sensing, increased tolerance  
 CC to sugars, altered carbon/nitrogen sensing, early flowering, late  
 CC flowering, altered flower structure, loss of flower determinacy, reduced  
 CC fertility, altered shoot meristem development, altered branching pattern,  
 CC altered stem morphology, altered vascular tissue structure, reduced  
 CC apical dominance, altered trichome density, altered trichome development,  
 CC altered trichome structure, altered root development, altered shade  
 CC germination, altered seed development, altered seed ripening, altered seed  
 CC germination, slow growth, fast growth, altered cell differentiation,  
 CC altered cell proliferation, altered cell expansion, altered phase change,  
 CC altered senescence, abnormal embryo development, altered programmed cell  
 CC death, lethality when overexpressed, altered necrosis patterns, increased  
 CC plant size, increased biomass, large seedlings, dwarfed plants, dark  
 CC green leaves, change in leaf shape, increased leaf size and mass, light  
 CC green or grey leaves, glossy leaves, altered abaxial/adaxial polarity,  
 CC altered seed coloration, altered seed size, altered seed shape, large  
 CC seed, increased leaf wax, increased leaf fatty acids, altered seed oil  
 CC content, altered seed protein content, altered seedprenyl content,  
 CC altered leaf prenyl lipid content, increased anthocyanin levels, and  
 CC decreased anthocyanin levels. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIP0 at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SO Sequence 174 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 Matches 86; Conservat 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINIRSMKCALPXNGKXXXXXXXXXAKDAKTXQECVSEFISPTSEASXKC 60  
 DB 27 REODRYLPINIRSMKCALPPNGK-----IAKDADKDTMOECVSEFISPTSEASBKC 79  
 QY 61 QXERKKTINGDDLMMAMATLGFEDYIEPLKVVYLXXYREXEG 101  
 DB 80 QXERKKTINGDDLMMAMATLGFEDYIEPLKVVYLARVREAGS 120  
 RESULT 7  
 ADS16958  
 ID ADS16958 standard; protein; 174 AA.  
 XX  
 AC ADS16958;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Plant polypeptide #17.  
 XX  
 KM Abiotic stress tolerance; LIL-related CCAAT transcription factor;  
 KM B domain; heat tolerance; drought stress tolerance; cold tolerance;  
 KM salt stress tolerance; MYB-related transcription factor;  
 KM seedling germination.  
 XX  
 OS Undentified.  
 XX  
 PN WO2004076638-A2.  
 PD 10-SEP-2004.  
 XX 25-FEB-2004; 2004WO-US005654.  
 PF 25-FEB-2003; 2003US-00374780.  
 PR 30-SEP-2003; 2003US-00675852.  
 XX  
 PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.  
 PI Sherman BK, Riechmann JL, Ratcliffe O, Jiang C, Heard JR;  
 PI Haake V, Creelman RA, Adam LJ, Reuber LT, Keddie JS, Dubell AN;  
 PI Plineda O, Repetti PP, Century KS, Guttersen NT, Yu G, Brown PE;  
 PI Kimimoto RW, Pilgrim ML;  
 DR WPI; 2004-653405/63.  
 XX  
 PT New transgenic plant having increased abiotic stress tolerance as  
 PT compared to non-transgenic plants of the same species, useful in  
 PT bioinformatic research methods.  
 PS Disclosure; Fig 10; 297bp; English.  
 XX  
 CC The invention relates to a transgenic plant having increased abiotic  
 CC stress tolerance as compared to non-transgenic plants of the same  
 CC species, where the transgenic plant comprises in its genome a transgene  
 CC encoding a polypeptide member of the G482 subclade of the non-LBEC1-like  
 CC clade of proteins of the LIL-related CCAAT transcription factor family,  
 CC where overexpression of the polypeptide member confers abiotic stress  
 CC tolerance. The invention also relates to a seed from the transgenic  
 CC plant, a method for producing a transgenic plant having increased  
 CC tolerance to abiotic stress comprising providing an expression vector  
 CC comprising the polynucleotide sequence encoding the polypeptide, and  
 CC regulatory elements operably linked to the nucleotide sequence, where the  
 CC regulatory elements are effective to control expression of the nucleotide  
 CC sequence in a target plant, introducing the expression vector into a  
 CC plant cell, growing the plant cell, allowing the plant to overexpress the  
 CC polypeptide and identifying one or more abiotic stress tolerant plants so  
 CC produced by comparing the one or more abiotic stress tolerant plants with  
 CC one or more non-transgenic plants of the same species, and a method for  
 CC increasing a plant's tolerance to abiotic stress comprising providing the

CC vector cited above and transforming the target plant with the vector to  
 CC generate a transformed plant with increased tolerance to abiotic stress.  
 CC compared to non-transgenic plants of the same species. The transgenic  
 CC plant comprises a polypeptide comprising a B domain. The B domain binds  
 CC to DNA at a transcription-regulating region comprising the motif CCAT, where  
 CC the binding regulates transcription of the DNA. The regulation of  
 CC transcription confers increased abiotic stress tolerance in the  
 CC transgenic plant as compared to non-transgenic plants of the same  
 CC species. The abiotic stress tolerance is selected from heat tolerance,  
 CC drought stress tolerance, cold tolerance and salt stress tolerance. The  
 CC transgenic plant further comprises a constitutive, inducible, or tissue-  
 CC specific promoter operably linked to the recombinant polynucleotide. The  
 CC recombinant polynucleotide is incorporated into an expression vector  
 CC comprising one or more regulatory elements that are effective to control  
 CC expression of the recombinant polynucleotide in a target plant. The  
 CC transgenic plant is a cultured host cell. The transgenic plant can  
 CC comprise in its genome a transgene encoding a polypeptide member of the  
 CC MB-related transcription factor family, where overexpression of the  
 CC polypeptide member confers abiotic stress tolerance. The transgenic plant  
 CC is useful in bioinformatic research methods. The invention provides  
 CC transgenic plants with improved seedling germination and performance  
 CC under conditions of limited nitrogen. This sequence represents a  
 CC polypeptide used in the scope of the invention.

CC Sequence 174 AA;

Query Match 92.3%; Score 423.5; DB 8; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 2.5e-54;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPIANISIRIMKALPXNGKXXXXXXIAKDAKXTXORCVSEFISFITSASXKC 60  
 DB 27 REODRYLPIANISIRIMKALPXNGK-----IAKDAKXTXORCVSEFISFITSASXKC 79

QY 61 QXERKRTINGDDLLMAMATGFEFDYIEPLKVLXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATGFEFDYIEPLKVLXXYREXEG 120

RESULT 8

ABG70264  
 ID ABG70264 standard; protein; 178 AA.

AC ABG70264;

XX 21-OCT-2002 (first entry)

DE IEC-1-related transcription factor polypeptide #17.

XX Maize; balsam pear; eucalyptus; rice; soybean; bread wheat; plant;

KM leafy cotyledon1-related transcription factor; plant embryogenesis;

KM LEC1-related transcription factor; thale cress; plant breeding.

OS Zea mays.

XX WO200257439-A2.

XX 25-JUL-2002.

XX 24-OCT-2001; 2001WO-US050908.

XX 24-OCT-2000; 2000US-0242739P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Cahoon RE, Klein TM;

XX WPI; 2002-590737/63.

PT New isolated polynucleotide encoding leafy cotyledon1-related  
 PT transcription factor, useful in facilitating studies for better  
 PT understanding of plant embryogenesis, or providing genetic tools for the  
 PT manipulation of plant growth.

XX Example 3; Fig 1; 63pp; English.

XX The invention relates to a polypeptide with leafy cotyledon1 (LEC1) -  
 CC related transcription factor activity and its associated polynucleotide.  
 CC The sequences are useful in facilitating studies for better understanding  
 CC of plant embryogenesis, and providing genetic tools for the manipulation  
 CC of plant growth. All or a substantial portion of the polynucleotides are  
 CC useful as probes for genetically and physically mapping the genes that  
 CC they are a part of, and as markers for traits linked to the genes, which  
 CC are useful in plant breeding to develop lines with desired phenotypes.  
 CC The probes may also be used in direct fluorescence in situ hybridisation  
 CC mapping. Sequences ABG70248-ABG70267 represent LEC1-related transcription  
 CC factor polypeptides of the invention

XX Sequence 178 AA;

Query Match 91.0%; Score 417.5; DB 5; Length 178;  
 Best Local Similarity 83.2%; Pred. No. 2e-53;  
 Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 REODRYLPIANISIRIMKALPXNGKXXXXXXIAKDAKXTXORCVSEFISFITSASXKC 60  
 DB 30 REODRYLPIANISIRIMKALPXNGK-----IAKDAKXTXORCVSEFISFITSASXKC 82

QY 61 QXERKRTINGDDLLMAMATGFEFDYIEPLKVLXXYREXEG 101  
 DB 83 QXERKRTINGDDLLMAMATGFEFDYIEPLKVLXXYREXEG 123

RESULT 9  
 ABR40821  
 ID ABR40821 standard; protein; 178 AA.

AC ABR40821;

XX 16-MAY-2003 (first entry)

DE Zea mays oil trait related protein sequence SEQ ID NO:413.

XX plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;

KM receptor-like protein kinase; mitogen activated protein kinase; oil;

KM LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;

KM CKC-like transcription factor; antisense inhibition; co-suppression;

XX transgenic plant.

OS Zea mays.

XX WO2003002751-A2.

XX 09-JAN-2003.

XX 27-JUN-2002; 2002WO-US020152.

XX 29-JUN-2001; 2001US-0301913P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT,

XX Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,

XX Tarczynski MC;

XX WPI; 2003-201509/19.

PT Novel nucleotide fragment encoding polypeptides having receptor-like  
 PT protein kinase activity, caleosin-like activity, useful for altering oil  
 PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.  
 PS Claim 12; Page 451; 542pp; English.  
 CC The present invention describes an isolated nucleotide fragment (1)  
 CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a

CC polypeptide (Pp) having receptor-like protein kinase activity, mitogen  
 CC activated protein (MAP)-kinase activity, LIPIS-like transcription factor  
 CC activity, calceosin-like activity, ATP citrate lyase activity, SNF1-like  
 CC activity, calceosin-like activity, transcription factor activity. Also described: (1)  
 CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or  
 CC (II), operably linked to a regulatory sequence; (3) a plant (IV)  
 CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)  
 CC oil obtained from (V). (I) or its part can be used in antisense  
 CC inhibition or co-suppression in a transformed plant. (III) is useful for  
 CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,  
 CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for  
 CC creating transgenic plants having altered lipid profiles. (I) can also be  
 CC used as a hybridisation probe. ACC00626 to ACC00668 and ABR40591 to  
 CC ABR40879 represent sequences used in the exemplification of the present  
 CC invention  
 CC  
 XX  
 SQ Sequence 178 AA;  
 Query Match 91.0%; Score 417.5; DB 6; Length 178;  
 Best Local Similarity 83.2%; Pred. No. 2e-53; Mismatches 8; Gaps 1;  
 Matches 84; Conservative 2; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSFFITSEASXKC 60  
 DB 30 REODRFLPINISIRIMKKAIPANGK-----IAKDAKXTXQECVSFFITSEASDKC 82  
 QY 61 QXERKRTINGDDLLMAMATGAFEDYIEPLKVLXXYREXEG 101  
 DB 83 QREKRTINGDDLLMAMATGAFEDYIEPLKVLXXYREXEG 123  
 RESULT 10  
 ADI42322  
 ID ADI42322 standard; protein; 178 AA.  
 XX  
 AC ADI42322;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Plant transcription factor #302.  
 XX  
 KW transgenic; plant; enhanced tolerance to abiotic stresses;  
 KW glycosylate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor; gene; ds.  
 XX  
 OS Zea mays.  
 XX  
 PN US2004019927-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 25-FEB-2003; 2003US-00374780.  
 XX  
 PR 18-APR-2001; 2001US-00837944.  
 XX  
 PA (SHER/) SHERMAN B. K.  
 PA (RIBC/) RIECHMANN J. L.  
 PA (CIAN/) JIANG C.  
 PA (HEAR/) HEARD J. E.  
 PA (HAAK/) HAAKE V.  
 PA (CREE/) CREELMAN R. A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L. J.  
 PA (REUB/) REUBER T. L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P. E.  
 PA (PILG/) PILGRIM M. L.

PA (DUBE/) DUBELL A. N.  
 PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.  
 XX  
 PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,  
 PI Riechmann RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,  
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
 XX  
 DR WPI: 2004-132245/13.  
 XX  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 XX  
 PS Claim 1, SEQ ID NO 785; 435bp; English.  
 XX  
 CC The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glycosylate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure, change in stem bifurcations, altered branching  
 CC pattern, reduced apical dominance, reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered trichome  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; seed morphology; seed  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This is the amino acid sequence of a plant  
 CC transcription factor, and an orthologue of Arabidopsis thaliana  
 CC transcription factors isolated in the invention, that can be used in the  
 CC creation of a transgenic plant with altered traits.  
 XX  
 SQ Sequence 178 AA;  
 Query Match 91.0%; Score 417.5; DB 8; Length 178;  
 Best Local Similarity 83.2%; Pred. No. 2e-53; Mismatches 8; Gaps 1;  
 Matches 84; Conservative 2; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSFFITSEASXKC 60  
 DB 30 REODRFLPINISIRIMKKAIPANGK-----IAKDAKXTXQECVSFFITSEASDKC 82  
 QY 61 QXERKRTINGDDLLMAMATGAFEDYIEPLKVLXXYREXEG 101  
 DB 83 QREKRTINGDDLLMAMATGAFEDYIEPLKVLXXYREXEG 123  
 RESULT 11  
 ADI42323  
 ID ADI42323 standard; protein; 179 AA.  
 XX  
 AC ADI42323;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Plant transcription factor #303.  
 XX  
 KW transgenic; plant; enhanced tolerance to abiotic stresses;  
 KW glycosylate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor; gene; ds.

OS Zea mays.

XX PN US2004019927-A1.

XX PD 29-JAN-2004.

XX PF 25-FEB-2003; 2003US-00374780.

XX PR 18-APR-2001; 2001US-00837944.

XX (SHER/) SHERMAN B. K.

XX (RIEC/) RIECHMANN J. L.

XX (JIANG/) JIANG C.

XX (HEAR/) HEARD J. E.

XX (HAAR/) HAARE V.

XX (CREE/) CREEHMAN R. A.

XX (RATC/) RATCLIFFE O.

XX (ADAM/) ADAM L. J.

XX (REUB/) REUBER T. L.

XX (KEDD/) KEDDIE J.

XX (BROU/) BROUN P. E.

XX (PILG/) PILGRIM M. L.

XX (DUBEL/) DUBELL A. N.

XX (PINE/) PINEDA O.

XX (YUGG/) YU G.

XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,

XX Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE,

XX Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX WPI; 2004-132245/13.

XX New transgenic plant comprising a recombinant polynucleotide of any one

XX PT of more than 500 nucleotide sequences, useful in bioinformatic search

XX methods.

XX Claim 1; SEQ ID NO 786; 435bp; English.

XX PS

XX XX

XX The invention describes a transgenic plant comprising a recombinant

XX CC polynucleotide of any one of more than 500 nucleotide sequences fully

XX CC defined in the specification or its complement. The method of the

XX CC invention can be used to produce a plant having altered traits such as:

XX CC enhanced tolerance to abiotic stress; glyphosate tolerance; hormone

XX CC sensitivity; disease resistance; sugar sensing; early or late flowering;

XX CC altered flower structure, change in stem bifurcations, altered branching

XX CC pattern, reduced apical dominance, reduced trichome density; lack of

XX CC trichomes; reduced ectopic trichome development; altered trichome

XX CC development; increase in trichome number; altered stem morphology;

XX CC increased root growth; increased root hairs; altered seed development;

XX CC altered cell proliferation or cell differentiation; rapid development;

XX CC premature senescence; increased necrosis; increase in seedling or plant

XX CC size; decreased plant size; leaf morphology; seed morphology; seed

XX CC biochemistry; increase in root anthocyanins; increase in plant

XX CC anthocyanins; or alteration in light response or shade avoidance. The

XX CC transgenic plant, polynucleotides and polypeptides are useful in

XX CC bioinformatic search methods. This is the amino acid sequence of a plant

XX CC transcription factor, and an orthologue of Arabidopsis thaliana

XX CC transcription factors isolated in the invention, that can be used in the

XX CC creation of a transgenic plant with altered traits.

XX SQ Sequence 179 AA;

XX Query Match 91.0%; Score 417.5; DB 8; Length 179;

XX Best Local Similarity 83.2%; Pred. No. 2e-53; Mismatches 8; Indels 7; Gaps 1;

XX Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

XX QY 1 REODRYLPINISIRIKKALPXNGKXXXXXXXXXAKDAKTXQBCVSEFISFITSBAKXC 60

XX Db 30 REODRFLPINISIRIKKALPANCK-----IAKDAKTXQBCVSEFISFITSBAKDC 82

XX QY 61 QREKRTKINGDDLLMAMATLGFEDYIEPLKVVYLXXYREXEG 101

XX Db 83 QREKRTKINGDDLLMAMATLGFEDYIEPLKVVYLQKREMEG 123

XX QY

XX Db

RESULT 12

ADCC23665 standard; protein; 290 AA.

AC ADCC23665;

XX

XX

DT 18-DEC-2003 (first entry)

XX

XX

XX

XX

XX

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RESULT 13

AAG04651 standard; protein; 141 AA.

AC AAG04651;

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XX AC AAG04651;  
XX 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 757.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridization assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
XX  
XX 25-FEB-1999; 99US-0121825P.  
XX 05-MAR-1999; 99US-0123180P.  
XX 09-MAR-1999; 99US-0123548P.  
XX 23-MAR-1999; 99US-0125788P.  
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PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161982P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 90.3%; Score 414.5; DB 3; Length 141;  
Best Local Similarity 81.2%; Pred. No. 4.1e-53;  
Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXAKDAKXTXOCVSEFFISFITSASXKC 60  
DB 20 REODRYLPINISIRIMKALPXNGK-----IGKDAKDTVOECVSEFFISFITSASDKC 72  
QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVLXXVREXEG 101  
DB 73 QXERKRTVNGDDLLMAMATLGFEDYIEPLKYLARRELEEG 113

RESULT 14  
ADE37175  
ID ADE37175 standard; protein; 141 AA.  
AC ADE37175;  
XX

DT 29-JAN-2004 (first entry)  
XX  
DE Plant yield related protein from clone G481.  
XX  
XX transcrption factor; tolerance; environmental condition;  
XX microbial disease; fungal disease; viral disease; pest infestation;  
XX herbicide sensitivity; heavy metal tolerance; heavy metal uptake;  
XX growth improvement; photocondition; nutrient uptake; hormone sensitivity;  
XX transgenic plant.  
XX  
OS Arabidopsis thaliana.  
XX  
XX  
PN MO2003014327-A2.  
XX  
XX 20-FEB-2003.  
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XX  
PF 09-AUG-2002; 2002MO-US026966.  
XX  
XX  
PR 09-AUG-2001; 2001US-0310847P.  
PR 19-NOV-2001; 2001US-0336049P.  
PR 11-DEC-2001; 2001US-0336692P.  
PR 14-JUN-2002; 2002US-00171468.  
XX  
XX (MEND-) MENDEL BIOTECHNOLOGY INC.  
XX  
XX Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;  
PI Reticliffe O, Pineda O, Yu GL, Brown PE,  
XX WPI; 2003-256576/25.  
XX  
XX N-PSDB; ADE37174.  
XX  
XX  
XX New stress-related transcription factor polynucleotides and polypeptides,  
PT useful for producing transgenic plants with e.g. improved tolerance to  
PT diseases or pests, decreased herbicide sensitivity, or improved nutrient  
PT uptake.  
XX  
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XX Disclosure; SEQ ID NO 114; 470bp; English.  
XX  
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XX The invention relates to a number of cDNA sequence and their encoded  
XX proteins which are especially transcription factor cDNAs and their  
XX proteins. The isolated or recombinant polynucleotide is useful for  
XX producing a modified plant with a modified trait, e.g. enhanced tolerance  
XX to environmental conditions, improved tolerance to microbial, fungal or  
XX viral diseases, improved tolerance to pest infestation, decreased  
XX herbicide sensitivity, improved tolerance of heavy metals, or enhanced  
XX ability to take up heavy metals, improved growth under poor  
XX photoconditions, improved nutrient uptake, or reduced hormone  
XX sensitivity. The transgenic plants are useful for growing a progeny plant  
XX comprising the desired trait. The polynucleotides and polypeptides are  
XX also useful in bioinformatic search methods. This sequence represents one  
XX of the proteins of the invention.  
XX  
SQ Sequence 141 AA;

Query Match 90.3%; Score 414.5; DB 7; Length 141;  
Best Local Similarity 81.2%; Pred. No. 4.1e-53;  
Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXAKDAKXTXOCVSEFFISFITSASXKC 60  
DB 20 REODRYLPINISIRIMKALPXNGK-----IGKDAKDTVOECVSEFFISFITSASDKC 72  
QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVLXXVREXEG 101  
DB 73 QXERKRTVNGDDLLMAMATLGFEDYIEPLKYLARRELEEG 113

RESULT 15  
ADF50740  
ID ADF50740 standard; protein; 141 AA.  
AC ADF50740;  
XX



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: November 17, 2005, 08:43:04 ; Search time 168 Seconds

(without alignments)  
307,857 Million cell updates/sec

Title: US-10-678-588a-8

Perfect score: 459

Sequence: 1 REODRVLPIANIRIMKAL.....FEDYIEPLKYLXXYREXEG 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARYS

Result No.	Score	Query Match	Length	DB ID	Description
1	417.5	91.0	167	2	084NF0
2	417.5	91.0	179	1	CBFA_MAIZE
3	414.5	90.3	141	2	09SLG0
4	407.5	88.8	176	2	067XJ2
5	407.5	88.8	228	2	09LFX3
6	402.5	87.7	173	2	08VYK4
7	400.5	87.3	161	2	023310
8	395.5	86.2	167	2	023634
9	395.5	86.2	190	2	09FGJ3
10	393.5	85.7	178	2	09ZQ03
11	388.5	84.6	152	2	084VE3
12	388.5	84.6	178	2	084NFI
13	388.5	84.6	189	2	0851T8
14	388.5	84.6	224	2	069J40
15	386.5	84.2	219	2	06YNK1
16	386.5	84.2	219	2	0751Z7
17	376.5	82.0	143	2	084NB9
18	376.5	82.0	215	2	09SIT9
19	366.5	79.8	241	2	065XK1
20	366.5	79.8	230	2	06YNK0
21	338.5	73.7	78	2	084K78
22	338.5	73.7	204	2	096WP0
23	337.5	73.5	148	2	063091
24	337.5	73.5	151	1	CBFA_CHICK
25	337.5	73.5	169	2	09D056
26	337.5	73.5	202	2	06MWJ9
27	337.5	73.5	206	2	06T2F0
28	337.5	73.5	207	1	CBFA_HUMAN
29	337.5	73.5	207	1	CBFA_MOUSE
30	337.5	73.5	207	1	CBFA_RAT
31	337.5	73.5	207	2	06RG77

32	337.5	73.5	224	2	08C590	08C590 mus musculus
33	336.5	73.3	186	2	000735	000735 emericella
34	336.5	73.3	206	2	06DD00	06DD00 xenopus lae
35	336.5	73.3	209	1	CBFA_PETMA	P25210 petromyzon
36	336.5	73.3	215	2	059848	059848 aspergillus
37	336.5	73.3	218	2	086ZV5	086ZV5 aspergillus
38	332.5	72.4	138	2	07PN95	07PN95 anopheles g
39	332.5	72.4	242	2	076256	076256 schistosoma
40	331.5	72.2	177	2	0942Y5	0942Y5 oryza sativ
41	330.5	72.0	206	2	073744	073744 xenopus lae
42	325.5	70.9	160	2	082248	082248 arabidopsis
43	325.5	70.9	197	2	08MO01	08MO01 strongyloce
44	324.5	70.7	194	2	06C1E2	06C1E2 yarrowia li
45	320.5	69.8	254	2	06YNJ7	06YNJ7 oryza sativ

## ALIGNMENTS

RESULT 1	ID	Q84NF0	PRELIMINARY;	PRT;	167 AA.
AC	Q84NF0				
DT	01-JUN-2003	(TREMUREl. 24, Created)			
DT	01-JUN-2003	(TREMUREl. 24, Last sequence update)			
DT	01-MAR-2004	(TREMUREl. 26, Last annotation update)			
DE	HAP3 (Fragment).				
GN	Name=Q84NF0B;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Emmatoidae; Oryzae; Oryza.				
OX	NCBI_TaxID=39947;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=2963257; PubMed=14617083;				
RA	Myoishi K., Ito Y., Serizawa A., Kurata N.;				
RT	"OSHAP3 genes regulate chloroplast biogenesis in rice."				
RL	Plant J. 36:532-540(2003).				
DR	EMBL; AB095439; BAC76332.1; -.				
DR	HSSP; P25208; INIJ.				
DR	Gramene; Q84NF0; -.				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003677; F:DNA binding; IEA.				
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.				
DR	InterPro; IPR003956; CBFA_NFYB.				
DR	InterPro; IPR003958; CBFA_NFYB domain.				
DR	InterPro; IPR003957; CBFA_NFYB_topis.				
DR	InterPro; IPR007124; Histone-fold.				
DR	InterPro; IPR007124; Histone-fold.				
DR	PIfam; PF00808; CBPD_NFYB_HMF.1.				
DR	PRINTS; PR00615; COATSUBUNITA.				
DR	PROSITE; PS00685; CBFA_NFYB; 1.				
FT	NON TER				
FT	1				
SQ	SEQUENCE 167 AA; 17971 MW; FB85544A22CE0495 CRC64;				
Query Match		91.0%; Score 417.5; DB 2; Length 167;			
Best local similarity		83.2%; Pred. No. 2.2e-45;			
Matches 84; Conservative		2; Mismatches 8; Indels 7; Gaps 1;			
Qy	1	REODRVLPIANIRIMKALPXXGKXXXXXIAKDAKTXQEVSHFISITSEASXKC 60			
Db	19	REODRVLPIANIRIMKALPANGK-----IAKAKTVOECVSHFISITSEASDKC 71			
Qy	61	QXERKTINGDDLLMAMATIGFEDYIEPLKYLXXYREXEG 101			
Db	72	QREKRTINGDDLLMAMATIGFEDYIEPLKYLXXYREXEG 112			
RESULT 2					
CBFA_MAIZE		STANDARD;	PRT;	179 AA.	
ID	P25205;				

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DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DB CCAAT-binding transcription factor subunit A (CBF-A) (NF- $\gamma$  protein
DE chain B) (NF- $\gamma$ B) (CAAT-box DNA binding protein subunit B).
GN Name:NFY2.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=92195809; PubMed=1549471;
RA Li X.-Y., Mantovani R., Hooft van Hujsdijnen R., Andre I.,
RA Benoist C., Mathis D.;
RT "Evolutionary variation of the CCAAT-binding transcription factor NF-
RT Y."
RL Nucleic Acids Res. 20:1087-1091(1992).
CC -1- FUNCTION: Stimulates the transcription of various genes by
CC recognizing and binding to a CCAAT motif in promoters, for example
CC in type I collagen, albumin and beta-actin genes.
CC -1- SUBUNIT: Heterotrimeric transcription factor composed of three
CC components, A, B and C. NF- $\gamma$ B and NF- $\gamma$ C must interact and dimerize
CC for NF- $\gamma$ A association and DNA binding.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: Can be divided into three domains: the weakly conserved A
CC domain, the highly conserved B domain thought to be involved in
CC subunit interaction and DNA binding, and the Glu-rich C domain.
CC -1- SIMILARITY: Belongs to the CBF-A subunit family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC CCB EMBL; X59714; CAA42234.1; -.
CC DR PIR; S22820; S22820.
CC DR HSSP; P25208; 1NIJ.
CC DR TRANSFAC; T05212; -.
CC DR Maizeda; 69282; -.
CC DR InterPro; IPR003956; CBF_A_NFYB.
CC DR InterPro; IPR003958; CBF_A_NFYB_domain.
CC DR InterPro; IPR003957; CBF_A_NFYB_topis.
CC DR InterPro; IPR007124; H1et_TAF.
CC DR InterPro; IPR009072; Histone-fold.
CC DR Pfam; PF00808; CBF_NFYB_HMF.1.
CC DR PRINTS; PR00615; CCAATSUBUNITA.
CC DR PROSITE; PS00685; CBF_A_NFYB; 1.
CC KW Activator; DNA-binding; Nuclear protein; Transcription regulation.
CC FT DOMAIN 1 29 A domain.
CC FT DOMAIN 30 119 B domain.
CC FT DNA_BIND 120 179 C domain.
CC FT SEQUENCE 179 AA; 18995 MW; 30621316CB46454 CRC64;
SQ
Query Match 91.0%; Score 417.5; DB 1; length 179;
Best Local Similarity 83.2%; Pred. No. 2,4e-45;
Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;
QY 1 REODRYVLIANTISRMKRLPVGNGGXXXXXXIADACKTQXQSCSEFISFTSEASKC 60
DB 30 REODRFLPLANISRLMKALIPNGK-----IADAKETVQSCSEFISFTSEASDK 82
QY 61 QXERKRTINGDDLWAMATLGFEDYIEPLKXVLIXXYREXEG 101
DB 83 QREKRTINGDDLWAMATLGFEDYIEPLKXVLIQYREXEG 123

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Q9SLG0		PRELIMINARY;	PRT;	141 AA.
ID	Q9SLG0			
AC	Q9SLG0, Q23633;			
DT	01-JUN-2000 (TrEMBLrel. 13, Created)			
DR	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Putative CCAAT-binding transcription factor subunit (Transcription factor).			
GN	Name=At2g38880; Synonym=s-hap3a;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.s.			
OK	NCBI TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,			
RA	Shen M., Ranning C.M., Fraser C.M., Somerville C.R., Venter J.C.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Town C.D., Kaul S.;			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RA	Edwards D., Smith A.G., Murray J.A.;			
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22088475; PubMed=12093376;			
RA	Hass B.J., Voliotovsky N., Town C.D., Troukhan M., Alexandrov N.,			
RA	Feldmann K.A., Flavell R.B., White O., Salzman S.L.;			
RT	"Full-length messenger RNA sequences greatly improve genome			
RT	annotation".			
RL	Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Brover J., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,			
RA	Feldmann K.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RA	Onodera K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,			
RA	Onodera C.S., Quach H.L., Tang C., Tortumt M., Wong C., Wu H.C.,			
RA	Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,			
RA	Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,			
RA	Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,			
RA	Soltisack A., Tripp M.G., Wu T., Shinzaki K., Davis R.W., Ecker J.R.,			
RA	Theologis A.;			
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RA	Yanada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,			
RA	Onodera C.S., Quach H.L., Tang C., Tortumt M., Wong C., Wu H.C.,			
RA	Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,			
RA	Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,			
RA	Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,			
RA	Soltisack A., Tripp M.G., Wu T., Shinzaki K., Davis R.W., Ecker J.R.,			
RA	Theologis A.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC0005770; AAC79602.2; -			
DR	EMBL; Y13723; CAAT4051.1; -			
DR	EMBL; AY088554; AAM65086.1; -			
DR	EMBL; BT004266; AAC42268.1; -			
DR	EMBL; BT005536; AA063956.1; -			
DR	PIR; B84810; B84810.			
DR	HSSP; P25208; INIJ.			
DR	TRANSFAC; T05198; -			
DR	ANT-2DPAGE; Q9SLG0; -			
DR	GO; GO:0005634; C:nucleus; IEA.			
DR	GO; GO:0003677; F:DNA binding; IEA.			
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.			
DR	InterPro; IPR003956; CBFA_NTFB.			

DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB\_topis.  
 DR InterPro: IPR003072; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB.1.  
 SQ SEQUENCE 141 AA; 15181 MW; D33060B5MD21D9E0 CRC64;

Query Match 90.3%; Score 414.5; DB 2; Length 141;  
 Best Local Similarity 81.2%; Pred. No. 4.5e-45;  
 Matches 82; Conservative 3; Mismatches 9; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISPTSEASXKC 60  
 Db 20 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISPTSEASDKC 72  
 Qy 61 QXERKKTNGDDLMAATLGFEDYIEPLKYLYLXXYREXEG 101  
 Db 73 QXERKKTNGDDLMAATLGFEDYIEPLKYLYLXXYREXEG 113

RESULT 4  
 067XJ2 PRELIMINARY; PRT; 176 AA.

AC 067XJ2; 28-10-2004 (TREMBlrel. 28, Created)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
 DE Transcription factor NF-Y, CCAAT-binding-like protein.  
 GN Name: A353340;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Totsuki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,  
 RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
 RA Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.  
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs";  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK176827; BAD44590.1; -.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB\_topis.  
 DR InterPro: IPR009072; Histone-fold.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB.1.  
 SQ SEQUENCE 176 AA; 19155 MW; 7F26A068342ED485 CRC64;

Query Match 88.8%; Score 407.5; DB 2; Length 176;  
 Best Local Similarity 80.2%; Pred. No. 4.5e-44;  
 Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISPTSEASXKC 60  
 Db 28 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISPTSEASDKC 80  
 Qy 61 QXERKKTNGDDLMAATLGFEDYIEPLKYLYLXXYREXEG 101  
 Db 81 QXERKKTNGDDLMAATLGFEDYIEPLKYLYLXXYREXEG 121

RESULT 5  
 09LF13 PRELIMINARY; PRT; 228 AA.  
 AC 09LF13;

DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Transcription factor NF-Y, CCAAT-binding-like protein.  
 GN Name: 74P12.40;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bloembergen H., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F.,  
 RA Salanoubat M.,  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Arabidopsis sequencing project;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL132966; CAB67641.1; -.  
 DR PIR: T45874; T45874.  
 DR HSHP: P25208; IN1J.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB\_topis.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF.1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB.1.  
 SQ SEQUENCE 228 AA; 25132 MW; BC158A80A08579B6 CRC64;

Query Match 88.8%; Score 407.5; DB 2; Length 228;  
 Best Local Similarity 80.2%; Pred. No. 5.9e-44;  
 Matches 81; Conservative 4; Mismatches 9; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISPTSEASXKC 60  
 Db 28 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQECVSEFISPTSEASDKC 80  
 Qy 61 QXERKKTNGDDLMAATLGFEDYIEPLKYLYLXXYREXEG 101  
 Db 81 QXERKKTNGDDLMAATLGFEDYIEPLKYLYLXXYREXEG 121

RESULT 6  
 08VYK4 PRELIMINARY; PRT; 173 AA.  
 ID 08VYK4;  
 AC 08VYK4; 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 03-JUN-2004 (TREMBlrel. 27, Last annotation update)  
 DE At2g37060/T2N18.18.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banb J.,  
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlton-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
 RA Yamamura Y., Yu G., Shinozaki K., Davis R.W., Theologis A.,  
 RA Becker J.R.,  
 RL Submitted (BSC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP SEQUENCE FROM N.A.  
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
RA Bower L., Carninci P., Chang B., Dale J.M., Goldsmith A.D.,  
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin U., Miranda M., Narusaka M.,  
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,  
RA Becker J.R.,  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY070477; AA149943.1; -.  
DR EMBL: AY091673; AA010272.1; -.  
DR HSSP: P25208; INTJ.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003677; P:DNA binding; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
DR PRINTS: PR00615; CCAATSUBNTA.  
DR PROSITE: PS00685; CBFA\_NFYB; 1.  
SQ SEQUENCE 173 AA; 1898 MW; 8C01E135B2DEC36A CRC64;  
Query Match 87.7%; Score 402.5; DB 2; Length 173;  
Best Local Similarity 79.2%; Pred. No. 1.9e-43;  
Matches 80; Conservative 4; Mismatches 10; Indels 7; Gaps 1;  
QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQSCVSFISFITSASXKC 60  
DB 29 REODRFLPINISIRIMKALPXNGK-----IAKDAKTXQSCVSFISFITSASXKC 81  
QY 61 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYXXYREXEG 101  
DB 82 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYXXYREXEG 122  
RESULT 7  
ID 023310 PRELIMINARY; PRT; 161 AA.  
AC 023310;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE CCAAT-binding transcription factor subunit A (CBF-A) (Putative CCAAT-  
binding transcription factor subunit A CBF-A) (At4g1540).  
GN Name=At3310w; Synonym=At4g1540; At4g1540/d13310w;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,  
RA Kreis M., Kavanagh T., Ertter K.D., Rieger M., Jones R.,  
RA Pridmore P., Hatzopoulos P., Obermaier B., Dueschhof A.,  
RA Jones J., Palme K., Ansgore W., Delseny M., Bancroft I., Mewes H.W.,  
RA Scheller C., Chalwatzis N.,  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Seti M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
RA Hayashizaki Y., Shinzaki K.,  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.

RA Shinn P., Chen H., Cheuk R., Kim C.J., Bower L., Carninci P.,  
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Huan V.W.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin U., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,  
RA Shinzaki K., Davis R.W., Theologis A., Becker J.R.,  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z97336; CAB10233.1; -.  
DR EMBL: AL161539; CAB78469.1; -.  
DR EMBL: AK117818; BAC42460.1; -.  
DR EMBL: BT003684; AAC39912.1; -.  
DR PIR: G71407; G71407.  
DR HSSP: P25208; INTJ.  
DR TRANSFAC: T05340; -.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003677; P:DNA binding; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR003956; CBFA\_NFYB.  
DR InterPro: IPR003958; CBFA\_NFYB domain.  
DR InterPro: IPR009072; Histone-fold.  
DR InterPro: IPR007124; Histone-fold.  
DR InterPro: IPR007124; Histone-fold.  
DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
DR PRINTS: PR00615; CCAATSUBNTA.  
DR PROSITE: PS00685; CBFA\_NFYB; 1.  
SQ SEQUENCE 161 AA; 17186 MW; 5C452E20D96A7AF4 CRC64;  
Query Match 87.3%; Score 400.5; DB 2; Length 161;  
Best Local Similarity 78.2%; Pred. No. 3.3e-43;  
Matches 79; Conservative 4; Mismatches 11; Indels 7; Gaps 1;  
QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKTXQSCVSFISFITSASXKC 60  
DB 20 REODRFLPINISIRIMKALPXNGK-----ISKDAKTXQSCVSFISFITSASXKC 72  
QY 61 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYXXYREXEG 101  
DB 73 QXERKTINGDDLLMAMATIGFEDYIEPLKYLYXXYREXEG 113  
RESULT 8  
ID 023634 PRELIMINARY; PRT; 187 AA.  
AC 023634;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Transcription factor (Fragment).  
GN Name=hap3;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Edwards D., Smith A.G., Murray J.A.,  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Y13724; CAA74052.1; -.  
DR HSSP: P25208; INTJ.  
DR TRANSFAC: T05195; -.  
DR GO: GO:0005634; C:nucleus; IEA.  
DR GO: GO:0003677; P:DNA binding; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR003956; CBFA\_NFYB.  
DR InterPro: IPR003958; CBFA\_NFYB domain.  
DR InterPro: IPR003957; CBFA\_NFYB top1.  
DR InterPro: IPR009072; Histone-fold.  
DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
DR PRINTS: PR00615; CCAATSUBNTA.  
DR PROSITE: PS00685; CBFA\_NFYB; 1.

FT NON TER 1 1  
SQ SEQUENCE 187 AA; 20295 MW; EAC7ABC9F37F408 CRC64;  
Query Match 86.2%; Score 395.5; DB 2; Length 187;  
Best Local Similarity 76.2%; Pred. No. 1.7e-42;  
Matches 77; Conservative 6; Mismatches 11; Indels 7; Gaps 1;  
Qy 1 REODRYPINANISIRIMKALPXNGKXXXXXXIAKDAXTKYQECVSEFISFTSEASXKC 60  
Db 23 REODRFLPIANVSHIMKALPANAK-----ISKDAETWQECVSEFISFTSEASDKC 75  
Qy 61 QXERKRTINGDDLMMATLGFEDYIEPLKYLLXXYREXG 101  
Db 76 QXERKRTINGDDLMMATLGFEDYIEPLKYLLQRFREIEG 116  
RESULT 9  
Q9FGJ3 PRELIMINARY; PRT; 190 AA.  
AC Q9FGJ3  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DE Similarity to CCAAT-box-binding transcription factor  
AT5947640/MN17.23.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_Taxid=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kaneke T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,  
RA Tabata S.; (APR-1999) to the EMBL/GenBank/DBJ databases.  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Ban J., Bowser L.,  
RA Carinci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
RA Lee J.M., Lin J., Miyazaki M., Narusaka M., Nguyen M., Onodera C.S.,  
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,  
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,  
RA Tracy S.E., Ban J., Bowser L., Carinci P., Chung M.K.,  
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,  
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,  
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,  
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,  
RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA EMBL; AB025628; BAB09050.1; -  
DR EMBL; AY078026; AAL7727.1; -  
DR EMBL; AF385744; AAK60334.1; -  
DR HSSP; P25208; IN1J.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR003957; CBFA\_NFYB domain.  
DR InterPro; IPR003958; CBFA\_NFYB domain.  
DR InterPro; IPR003957; CBFA\_NFYB domain.  
DR InterPro; IPR003957; CBFA\_NFYB domain.  
DR InterPro; IPR007124; Histone-fold.  
DR InterPro; IPR007124; Histone-fold.  
DR Pfam; PF00808; CBFA\_NFYB\_HNF; 1.  
DR PRINTS; PR00615; CCAATSUBUNTA.  
DR PROSITE; PS00685; CBFA\_NFYB; 1.  
SQ SEQUENCE 190 AA; 20529 MW; DBSC0F4247C02 CRC64;

Query Match 86.2%; Score 395.5; DB 2; Length 190;  
Best Local Similarity 76.2%; Pred. No. 1.7e-42;  
Matches 77; Conservative 6; Mismatches 11; Indels 7; Gaps 1;  
Qy 1 REODRYPINANISIRIMKALPXNGKXXXXXXIAKDAXTKYQECVSEFISFTSEASXKC 60  
Db 26 REODRFLPIANVSHIMKALPANAK-----ISKDAETWQECVSEFISFTSEASDKC 78  
Qy 61 QXERKRTINGDDLMMATLGFEDYIEPLKYLLXXYREXG 101  
Db 79 QXERKRTINGDDLMMATLGFEDYIEPLKYLLQRFREIEG 119  
RESULT 10  
Q9ZQC3 PRELIMINARY; PRT; 178 AA.  
AC Q9ZQC3  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DE Similarity to CCAAT-box binding transcription factor.  
GN Name=At2g37060;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_Taxid=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanKen S.B.,  
RA Barnstead M.B., Mason T.M., Bowman C.L., Roming C.M., Banto M.-I.,  
RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,  
RA Fraser C.M., Venter J.C.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Town C.D., Kaul S.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA EMBL; AC006260; AADI8153.1; -  
DR PIR; A84788; A84788.  
DR HSSP; P25208; IN1J.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR003957; CBFA\_NFYB domain.  
DR InterPro; IPR003958; CBFA\_NFYB domain.  
DR InterPro; IPR003957; CBFA\_NFYB domain.  
DR InterPro; IPR003957; CBFA\_NFYB domain.  
DR InterPro; IPR007124; Histone-fold.  
DR InterPro; IPR007124; Histone-fold.  
DR Pfam; PF00808; CBFA\_NFYB\_HNF; 1.  
DR PRINTS; PR00615; CCAATSUBUNTA.  
DR PROSITE; PS00685; CBFA\_NFYB; 1.  
SQ SEQUENCE 178 AA; 19523 MW; B3CF497383EC86C4 CRC64;  
Query Match 85.7%; Score 393.5; DB 2; Length 178;  
Best Local Similarity 76.0%; Pred. No. 2.9e-42;  
Matches 78; Conservative 5; Mismatches 10; Indels 7; Gaps 1;  
Qy 1 REODRYPINANISIRIMKALPXNGKXXXXXXIAKDAXTKYQECVSEFISFTSEASXKC 60  
Db 29 REODRFLPIANVSHIMKALPANAK-----ISKDAETWQECVSEFISFTSEASDKC 81  
Qy 61 QXERKRTINGDDLMMATLGFEDYIEPLKYLLXXYREXG 100  
Db 82 QXERKRTINGDDLMMATLGFEDYIEPLKYLLQRFREIEG 121  
RESULT 11  
Q84VF3 PRELIMINARY; PRT; 152 AA.  
AC Q84VF3  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DB CCAAT-binding transcription factor-like protein (Fragment).  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 ON NCBI\_Taxid=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2311120; PubMed=14750518;  
 RX DOI=10.1023/B:PLAN.000007001.30865.0f;  
 RA Cooper B., Hutchison D., Park S., Guimil S., Lugimbuhl P., Ellero C.,  
 RA Goff S.A., Glazebrook J.;  
 RT "Identification of rice (*Oryza sativa*) proteins linked to the cyclin-  
 RT mediated regulation of the cell cycle.";  
 RL Plant Mol. Biol. 53:273-279(2003).  
 DR EMBL: AY224530; AAO72650.1; -.  
 DR HSSP: P25208; 1MJT.  
 DR Gramene; Q84VF3; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003957; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1e.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB; 1.  
 FT NON TER 1  
 SQ SEQUENCE 152 AA; 16456 MW; 89EB826AD6124EFB CRC64;  
 Query Match 84.6%; Score 388.5; DB 2; Length 152;  
 Best Local Similarity 83.2%; Pred. No. 1.1e-41;  
 Matches 79; Conservative 1; Mismatches 8; Indels 7; Gaps 1;  
 QY 7 LPIANISRIKMKALPXXGKXXXXXXIAKDAKXTQECVSEFISFITSASXKCQXKRRK 66  
 DB 10 LPIANISRIKMKALPXXGK-----IAKDAKXTQECVSEFISFITSASXKCQXKRRK 62  
 QY 67 TINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
 DB 63 TINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 97  
 RESULT 12  
 Q84NFI PRELIMINARY; PRT; 178 AA.  
 AC Q84NFI;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE HAP3.  
 GN Name=OSHAP3A;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 ON NCBI\_Taxid=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22983257; PubMed=14617083;  
 RA Miyoshi K., Ito Y., Serizawa A., Kurata N.;  
 RT "OSHAP3 genes regulate chloroplast biogenesis in rice.";  
 RL Plant J. 36:532-540(2003).  
 DR EMBL: AB095438; BAC76331.1; -.  
 DR HSSP: P25208; 1MJT.  
 DR Gramene; Q84NFI; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.

DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1e.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.  
 DR PRINTS: PR00615; CCAATSUBUNTA.  
 DR PROSITE: PS00685; CBFA\_NFYB; 1.  
 SQ SEQUENCE 178 AA; 19200 MW; 1D620383B9E82926 CRC64;  
 Query Match 84.6%; Score 388.5; DB 2; Length 178;  
 Best Local Similarity 75.2%; Pred. No. 1.3e-41;  
 Matches 76; Conservative 9; Mismatches 9; Indels 7; Gaps 1;  
 QY 1 REODRYLPIANISRIKMKALPXXGKXXXXXXIAKDAKXTQECVSEFISFITSASXKC 60  
 DB 33 REODRYLPIANISRIKMKALPXXGK-----IAKDAKXTQECVSEFISFITSASXKC 85  
 QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 101  
 DB 86 QXERKRTINGDDLLMAMATLGFEDYIEPLKVIYLYXXYREXEG 126  
 RESULT 13  
 Q851T8 PRELIMINARY; PRT; 189 AA.  
 AC Q851T8;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE Putative CAAT-box DNA binding protein (CCAAT-binding protein).  
 GN Name=P0506B12.4; Synonyma=CCB1, P0460C04.24;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriactoidae; Oryzaceae; Oryza.  
 ON NCBI\_Taxid=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12447438; DOI=10.1038/nature01184;  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Karamori H.,  
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
 RA Hijiwata S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuuchi A., Kamuya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Yama H., Endo T., Ito H., Hahn J.H., Kim H.I., Sun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yao Q., Peng R., Xiong A.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP003271; BAB89732.1; -.  
 DR EMBL: AP004366; BAB92931.1; -.  
 DR EMBL: AY32466; AAO01152.1; -.  
 DR HSSP: P25208; 1MJT.  
 DR Gramene; Q851T8; -.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR003956; CBFA\_NFYB.  
 DR InterPro: IPR003958; CBFA\_NFYB domain.  
 DR InterPro: IPR003957; CBFA\_NFYB top1e.  
 DR InterPro: IPR009072; Histone-fold.  
 DR InterPro: IPR007124; Hist\_TAF.  
 DR Pfam: PF00808; CBFD\_NFYB\_HMF; 1.

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DR PRINTS: PRO0615; CCAATSUBUNTA.
DR PROSITE; PS00685; CBFA_NFYB; 1.
SQ SEQUENCE 189 AA; 20752 MW; 0D385703DACS25D3 CRC64;

Query Match
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Matches 76; Conservative 9; Mismatches 9; Indels 7; Gaps 1;

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DB 19 REODRFLPININISIRIMKAVPANAK-----IAKDAKETVQECVSEFISFITSASDKC 71

QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVTLYXXYREXEG 101
DB 72 QXERKRTINGEDLLFMATLGFEDYVDPKHTLHKFRELEG 112

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AC Q69J40;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative transcription factor.
GN Name=OSUNBA0072106.11; Synonyms=P0493C06.26;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa n Japonbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OSUNBA0072106.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa n Japonbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0493C06.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006458; BAD32022.1; -.
DR EMBL; AP005193; BAD31143.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003956; CBFA_NFYB.
DR InterPro; IPR003958; CBFA_NFYB_domain.
DR InterPro; IPR003957; CBFA_NFYB_topls.
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR007124; Hist_TAF.
DR Pfam; PF00808; CBFD_NFYB_HMF.1.
DR PRINTS; PRO0615; CCAATSUBUNTA.
DR PROSITE; PS00685; CBFA_NFYB; 1.
SQ SEQUENCE 224 AA; 23273 MW; D2E32DC64D138BBF CRC64;

Query Match
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Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

QY 1 REODRYPININISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60
DB 21 REODRFLPININISIRIMKALPANAK-----ISKDAKETVQECVSEFISFITSASDKC 73

QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVTLYXXYREXEG 101
DB 74 QXERKRTINGDDLLMAMATLGFEDYVDPKHTLHKFRELEG 114

RESULT 15
Q6VYK1

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DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE HAP3-like transcriptional-activator.
GN Name=HAP3;
OS Oryza sativa (Indica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxId=39946;
RN [1]
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa n Japonbare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OSUNBA0072106.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY062181; AAL47206.1; -.
DR HSRP; P19267.1A7W.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003956; CBFA_NFYB.
DR InterPro; IPR003958; CBFA_NFYB_domain.
DR InterPro; IPR003957; CBFA_NFYB_topls.
DR InterPro; IPR009072; Histone-fold.
DR InterPro; IPR007124; Hist_TAF.
DR Pfam; PF00808; CBFD_NFYB_HMF.1.
DR PRINTS; PRO0615; CCAATSUBUNTA.
DR PROSITE; PS00685; CBFA_NFYB; 1.
SQ SEQUENCE 219 AA; 22387 MW; 704BD8B9E0C5F2C0 CRC64;

Query Match
Best Local Similarity 84.2%; Score 386.5; DB 2; Length 219;
Matches 76; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

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DB 23 REODRFLPININISIRIMKALPANAK-----ISKDAKETVQECVSEFISFITSASDKC 75

QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVTLYXXYREXEG 101
DB 76 QXERKRTINGDDLLMAMATLGFEDYVDPKHTLHKFRELEG 116

Search completed: November 17, 2005, 08:55:33
Job time: 170 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2005, 08:46:10 ; Search time 25 Seconds

(Without alignments)  
301.582 Million cell updates/sec

Title: US-10-678-588A-8

Perfect score: 459

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
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2: /cgn2\_6/proddata/1/1aa/5B COMB pep: \*  
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4: /cgn2\_6/proddata/1/1aa/6B COMB pep: \*  
5: /cgn2\_6/proddata/1/1aa/6C COMB pep: \*  
6: /cgn2\_6/proddata/1/1aa/backfile1 pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	402.5	87.7	90	3	US-09-103-478-20	Sequence 20, Appl
2	402.5	87.7	90	3	US-09-193-931C-20	Sequence 20, Appl
3	402.5	87.7	90	4	US-09-516-052-30	Sequence 30, Appl
4	401.5	86.6	218	4	US-09-828-303-23	Sequence 23, Appl
5	397.5	86.6	219	4	US-09-640-211A-1051	Sequence 1051, Ap
6	337.5	73.5	207	4	US-09-538-092-1008	Sequence 1008, Ap
7	337.5	73.5	211	4	US-09-949-016-7348	Sequence 7348, Ap
8	332.5	72.4	90	3	US-09-103-478-21	Sequence 21, Appl
9	332.5	72.4	90	3	US-09-103-478-24	Sequence 24, Appl
10	332.5	72.4	90	3	US-09-103-478-25	Sequence 25, Appl
11	332.5	72.4	90	3	US-09-193-931C-21	Sequence 21, Appl
12	332.5	72.4	90	3	US-09-193-931C-24	Sequence 24, Appl
13	332.5	72.4	90	3	US-09-193-931C-25	Sequence 25, Appl
14	332.5	72.4	90	4	US-09-516-052-31	Sequence 31, Appl
15	332.5	72.4	90	4	US-09-516-052-34	Sequence 34, Appl
16	332.5	72.4	90	4	US-09-516-052-35	Sequence 35, Appl
17	331.5	72.2	90	3	US-09-103-478-22	Sequence 22, Appl
18	331.5	72.2	90	3	US-09-193-931C-22	Sequence 22, Appl
19	331.5	72.2	90	3	US-09-516-052-32	Sequence 32, Appl
20	329.5	71.8	90	3	US-09-103-478-26	Sequence 26, Appl
21	329.5	71.8	90	3	US-09-193-931C-26	Sequence 26, Appl
22	329.5	71.8	90	4	US-09-516-052-36	Sequence 36, Appl
23	323.5	70.5	146	4	US-09-435-054A-8	Sequence 8, Appl
24	323.5	70.5	240	4	US-09-435-054A-10	Sequence 10, Appl
25	323.5	70.3	355	4	US-09-435-054A-18	Sequence 18, Appl
26	322.5	70.3	214	4	US-09-435-054A-12	Sequence 12, Appl
27	319.5	69.6	205	4	US-09-516-052-20	Sequence 20, Appl

28	319.5	69.6	216	4	US-09-516-052-22	Sequence 22, Appl
29	317.5	69.2	108	4	US-09-640-211A-1174	Sequence 1174, Ap
30	316.5	69.0	278	4	US-09-435-054A-2	Sequence 2, Appl
31	315.5	68.7	109	4	US-09-248-796A-18639	Sequence 18639, A
32	308.5	67.2	208	3	US-09-103-478-2	Sequence 2, Appl
33	308.5	67.2	208	3	US-09-193-931C-2	Sequence 2, Appl
34	308.5	67.2	208	4	US-09-026-221-2	Sequence 2, Appl
35	308.5	67.2	208	4	US-09-538-029-70	Sequence 70, Appl
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38	299.5	65.3	90	3	US-09-103-478-19	Sequence 19, Appl
39	299.5	65.3	90	3	US-09-193-931C-19	Sequence 19, Appl
40	299.5	65.3	90	4	US-09-516-052-29	Sequence 29, Appl
41	294.5	64.2	121	4	US-09-270-767-59691	Sequence 59691, A
42	294.5	64.2	164	4	US-09-270-767-44270	Sequence 44270, A
43	288.5	62.9	108	4	US-09-640-211A-1090	Sequence 1090, Ap
44	288.5	62.9	144	3	US-09-319-989-4	Sequence 4, Appl
45	288.5	62.9	144	4	US-09-538-092-15	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
US-09-103-478-20

Sequence 20, Application US/09103478  
Patent No. 6235975

GENERAL INFORMATION:

APPLICANT: Harada, John

APPLICANT: Lotan, Tamar

APPLICANT: Ocho, Masa-aki

APPLICANT: Goldberg, Robert B.

APPLICANT: Fischer, Robert L.

TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESSES:

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COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/103,478

FILING DATE: 24-JUN-1998

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026,221

FILING DATE: 19-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/804,534

FILING DATE: 21-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Blinhorst, Gregory P.

REGISTRATION NUMBER: 38,440

REFERENCE/DOCKET NUMBER: 023070-077611US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-103-478-20

Query Match 87.7%; Score 402.5; DB 3; Length 90;  
Best Local Similarity 83.5%; Pred. No. 3.9e-52;  
Matches 81; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTQCVSEFFISFITSASXKC 60  
DB 1 REODRFLPINISIRIMKALPANCK-----IAKDAKXTQCVSEFFISFITSASDKC 53

QY 61 QXERKTINGDDLLMAMATGFEFDYIEPLKVLXXYR 97  
DB 54 QXERKTINGDDLLMAMATGFEFDYIEPLKVLQKTR 90

RESULT 2  
US-09-193-931C-20  
Sequence 20, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C  
CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 20  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURES:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: maize HAP3 subunit of CCAAT box-binding factor  
OTHER INFORMATION: (CBF) protein B domain homolog  
US-09-193-931C-20

Query Match 87.7%; Score 402.5; DB 3; Length 90;  
Best Local Similarity 83.5%; Pred. No. 3.9e-52;  
Matches 81; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTQCVSEFFISFITSASXKC 60  
DB 1 REODRFLPINISIRIMKALPANCK-----IAKDAKXTQCVSEFFISFITSASDKC 53

QY 61 QXERKTINGDDLLMAMATGFEFDYIEPLKVLXXYR 97  
DB 54 QXERKTINGDDLLMAMATGFEFDYIEPLKVLQKTR 90

RESULT 3  
US-09-516-052-30  
Sequence 30, Application US/09516052  
Patent No. 6781035  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
APPLICANT: Bul, Anhthu  
APPLICANT: Khong, Raymond  
APPLICANT: The Regents of the University of California

TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077630US  
CURRENT APPLICATION NUMBER: US/09/516,052  
CURRENT FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US 09/193,931  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 30  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURES:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: maize HAP3 subunit of CCAAT box-binding factor  
OTHER INFORMATION: (CBF) protein B domain homolog  
US-09-516-052-30

Query Match 87.7%; Score 402.5; DB 4; Length 90;  
Best Local Similarity 83.5%; Pred. No. 3.9e-52;  
Matches 81; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTQCVSEFFISFITSASXKC 60  
DB 1 REODRFLPINISIRIMKALPANCK-----IAKDAKXTQCVSEFFISFITSASDKC 53

QY 61 QXERKTINGDDLLMAMATGFEFDYIEPLKVLXXYR 97  
DB 54 QXERKTINGDDLLMAMATGFEFDYIEPLKVLQKTR 90

RESULT 4  
US-09-828-303-23  
Sequence 23, Application US/09828303  
Patent No. 6677504  
GENERAL INFORMATION:  
APPLICANT: COSTA E SILVA, OSMALDO DA  
APPLICANT: BOHNER, HANS J.  
APPLICANT: VAN THIESEN, NOCHA  
APPLICANT: CHEN, RUDYING  
TITLE OF INVENTION: TRANSCRIPTION FACTOR STRESS-RELATED PROTEINS AND  
TITLE OF INVENTION: METHODS OF USE IN PLANTS  
FILE REFERENCE: 16313-0030  
CURRENT APPLICATION NUMBER: US/09/828,303  
CURRENT FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: 60/196,001  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 23  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Physcomitrella patens  
US-09-828-303-23

Query Match 87.5%; Score 401.5; DB 4; Length 218;  
Best Local Similarity 78.2%; Pred. No. 1.7e-51;  
Matches 79; Conservative 5; Mismatches 10; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXXXXIAKDAKXTQCVSEFFISFITSASXKC 60  
DB 34 REODRFLPINISIRIMKALPSNAK-----ISKDAKXTQCVSEFFISFITSASDKC 86

QY 61 QXERKTINGDDLLMAMATGFEFDYIEPLKVLXXYREXEG 101  
DB 87 QXERKTINGDDLLMAMSTLGFEFDYIEPLKVLHRYELBG 127

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RESULT 5
US-09-640-211A-1051
; Sequence 1051, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modifications and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1051
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-640-211A-1051

Query Match      86.6%; Score 397.5; DB 4; Length 219;
Best Local Similarity 75.2%; Pred. No. 6.8e-51;
Matches 76; Conservative 7; Mismatches 11; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQECVSEFISFTSEASXKC 60
Db 24 KEDRFLPINVAGIMKALPANCK-----VSKAKETVQECVSEFISFTSEASDKC 76
Qy 61 QXERKTINGDDILMAMATIGFEDYIEPLKYLLXXYREXG 101
Db 77 QXERKTINGDDILMAMATIGFEDYIEPLKYLLXXYREMEG 117

RESULT 6
US-09-538-092-1008
; Sequence 1008, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1008
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P25208
US-09-538-092-1008

Query Match      73.5%; Score 337.5; DB 4; Length 207;
Best Local Similarity 67.3%; Pred. No. 5.5e-42;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQECVSEFISFTSEASXKC 60
Db 53 REODIYLPINAVARIMKALPQTK-----IAKDAKCVQECVSEFISFTSEASERC 105
Qy 61 QXERKTINGDDILMAMATIGFEDYIEPLKYLLXXYRE 98

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Db 106 HOERKTINGEDILFAMSTIGFDSYVEPLKYLLQKPRE 143

RESULT 7
US-09-949-016-7348
; Sequence 7348, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7348
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7348

Query Match      73.5%; Score 337.5; DB 4; Length 211;
Best Local Similarity 67.3%; Pred. No. 5.7e-42;
Matches 66; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTQECVSEFISFTSEASXKC 60
Db 56 REODIYLPINAVARIMKALPQTK-----IAKDAKCVQECVSEFISFTSEASERC 108
Qy 61 QXERKTINGDDILMAMATIGFEDYIEPLKYLLXXYRE 98
Db 109 HOERKTINGEDILFAMSTIGFDSYVEPLKYLLQKPRE 146

RESULT 8
US-09-103-478-21
; Sequence 21, Application US/09103478
; Patent No. 6235975
; GENERAL INFORMATION:
; APPLICANT: Harada, John
; APPLICANT: Lotan, Tamar
; APPLICANT: Ohto, Masa-aki
; APPLICANT: Goldberg, Robert B.
; APPLICANT: Fischer, Robert L.
; TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,478
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,221
; FILING DATE: 19-FEB-1998

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-21

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1,1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRINKALPXNGKXXXXXXXXXAKDAKXTXQCVSEFFISFITSASXKC 60  
DB 1 REODIYLPINAVARINKMAIPQTGK-----IAKDAKECVQECVSEFFISFITSASERC 53  
QY 61 QXERKRTINGDDILMAMATGTFEDYIEPLKVTLYLXXR 97  
DB 54 HQERKRTINGEDILFAMSTLGFQSYVEPLKLYLQKFR 90

## RESULT 9

US-09-103-478-24  
Sequence 24, Application US/09103478  
Patent No. 6235975  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohno, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,478  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,221  
FILING DATE: 19-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-24

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1,1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRINKALPXNGKXXXXXXXXXAKDAKXTXQCVSEFFISFITSASXKC 60  
DB 1 REODIYLPINAVARINKMAIPQTGK-----IAKDAKECVQECVSEFFISFITSASERC 53  
QY 61 QXERKRTINGDDILMAMATGTFEDYIEPLKVTLYLXXR 97  
DB 54 HQERKRTINGEDILFAMSTLGFQSYVEPLKLYLQKFR 90

## RESULT 10

US-09-103-478-25  
Sequence 25, Application US/09103478  
Patent No. 6235975  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohno, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,478  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,221  
FILING DATE: 19-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/804,534  
FILING DATE: 21-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-077611US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-103-478-25

Query Match 72.4%; Score 332.5; DB 3; Length 90;

Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINVARIMNGALPQTGK-----IAKDAKCEVCQECVSEFISFITSASBRC 53

QY 61 QXERKRTINGDDLLMAMATGFEEDYIRPLKYLKXXR 97  
Db 54 HQERKRTINGEDILFAMSTLGFOSYVEPLKYLQKFR 90

RESULT 11  
US-09-193-931C-21  
Sequence 21, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C  
CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 21  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Gallus sp.  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: chicken HAP3 subunit of CCAAT box-binding factor  
US-09-193-931C-21

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINVARIMNGALPQTGK-----IAKDAKCEVCQECVSEFISFITSASBRC 53  
QY 61 QXERKRTINGDDLLMAMATGFEEDYIRPLKYLKXXR 97  
Db 54 HQERKRTINGEDILFAMSTLGFOSYVEPLKYLQKFR 90

RESULT 12  
US-09-193-931C-24  
Sequence 24, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C

CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: human HAP3 subunit of CCAAT box-binding factor  
US-09-193-931C-24

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQECVSEFISFITSASXKC 60  
Db 1 REODIYLPINVARIMNGALPQTGK-----IAKDAKCEVCQECVSEFISFITSASBRC 53  
QY 61 QXERKRTINGDDLLMAMATGFEEDYIRPLKYLKXXR 97  
Db 54 HQERKRTINGEDILFAMSTLGFOSYVEPLKYLQKFR 90

RESULT 13  
US-09-193-931C-25  
Sequence 25, Application US/09193931C  
Patent No. 6320102  
GENERAL INFORMATION:  
APPLICANT: Harada, John  
APPLICANT: Lotan, Tamar  
APPLICANT: Ohto, Masa-aki  
APPLICANT: Goldberg, Robert B.  
APPLICANT: Fischer, Robert L.  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: LEAFY COTYLEDON1 Genes and Their Uses  
FILE REFERENCE: 023070-077620  
CURRENT APPLICATION NUMBER: US/09/193,931C  
CURRENT FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: US 09/103,478  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: US 09/026,221  
PRIOR FILING DATE: 1998-02-19  
PRIOR APPLICATION NUMBER: US 08/804,534  
PRIOR FILING DATE: 1997-02-21  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 25  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Mus musculus and Rattus norvegicus  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (1)..(90)  
OTHER INFORMATION: mouse/rat HAP3 subunit of CCAAT box-binding factor  
US-09-193-931C-25

Query Match 72.4%; Score 332.5; DB 3; Length 90;  
Best Local Similarity 67.0%; Pred. No. 1.1e-41;  
Matches 65; Conservative 12; Mismatches 13; Indels 7; Gaps 1;

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D6      1 REODIYLPANVARIMGNALPQTSK-----IAKAKEVCQECSVEFISPTISEASERC 54
Q7      61 QXERKTINDDDLMMATIGFEDEYEPLKYLLXXR 97
          |||||:::||:||||:||||:||||:|:|:|
D8      54 HQERKTINGEDILPMSTLGFQSYVPEPLYLQKPR 90
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RESULT 14  
US-09-516-052-31

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Sequence 31, Application US/09516052
Patent No. 6781035
GENERAL INFORMATION:
APPLICANT: Harada, John
APPLICANT: Lotan, Tamar
APPLICANT: Ono, Masa-Aki
APPLICANT: Goldberg, Robert B.
APPLICANT: Fischer, Robert L.
APPLICANT: Bul, Anshun
APPLICANT: Kiong, Raymond
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: LEADY COTYPEPON1 Genes and Their Uses
FILE REFERENCE: 023070-077630US
CREATOR: ABEI,JOHN;JON YUENP,UCB/06/05/cr_0cc

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/ SEQ ID NO 31
/ LENGTH: 90
/ TYPE: PRT
/ ORGANISM: Gallus sp.
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (1)..(90)
/ OTHER INFORMATION: chicken HspA subunit of CCAAT box-binding factor
/ OTHER INFORMATION: (CBF) protein B domain homolog
US-09-516-052-31

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Best Local Similarity	67.0%;	Pred. NO.	1.1e-41;				
Matches	65;	Conservative	12;	Mismatches	13;	Indels	7;
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Qy      61 QXKRKTINGDDLWMATLGFEDYIEPLKVLXXRR 97
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RESULT 15
US-09-516-052-34
: Sequence 34: Application US/09516052
: Patent No. 6781035
: GENERAL INFORMATION:
: APPLICANT: Harada, John
: APPLICANT: Lotan, Tamara
: APPLICANT: Ohno, Masa-Aki
: APPLICANT: Goldberg, Robert B.
: APPLICANT: Fischer, Robert L.
: APPLICANT: Bul, Anshu
: APPLICANT: Khong, Raymond
: TITLE OF INVENTION: The Regents of the University of California
: FILE REFERENCE: 023070-077630US

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CURRENT APPLICATION NUMBER: US/09/516,052
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 09/193,931
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: US 09/103,478
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: US 09/026,221
PRIOR FILING DATE: 1998-02-19
PRIOR APPLICATION NUMBER: US 08/804,534
PRIOR FILING DATE: 1997-02-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 90
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (1)..(90)
OTHER INFORMATION: human HAP3 subunit of CCAAT Box-binding factor3
OTHER INFORMATION: (CBF) protein B domain homolog
US-09-516-052-34

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Query Match	72.4%;	Score 332.5;	DB 4;	Length 90;
Best Local Similarity	67.0%;	Pred. No. 1.1e-41;		
Matches	65;	Conservative	12;	Mismatches 13;
				Indels 7;
				Gaps 1;

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Db       1 RQGDVPLPAINVARIMKNALPGTK-----IADKAECVQECSEFISFTSASERC 533
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QY      61 QXKRKTINGDDLLMAMATLGFEIDYIEPLKVLXXR   97
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Db      54 HQEKRKTINGEDLLFAMSTLGFQSYVEPLKYLQFR   90
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Search completed: November 17, 2005, 08:56:02  
Job time : 26 secs

Search completed: November 17, 2005, 08:56:02  
Job time : 26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2005, 08:52:50 / Search time 165 Seconds

(without alignments)  
256.117 Million cell updates/sec

Title: US-10-678-588A-8

Perfect score: 459

Sequence: 1 REGDRLVPIINIRIMKKAL.....FEDYIEPLKYLXXYREXG 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	425	92.6	185	17	US-10-675-852-42
4	423.5	92.3	160	15	US-10-374-780A-802
5	423.5	92.3	160	17	US-10-675-852-26
6	423.5	92.3	173	15	US-10-424-599-274836
7	423.5	92.3	173	17	US-10-678-588A-6
8	423.5	92.3	173	17	US-10-675-852-24
9	423.5	92.3	174	15	US-10-424-599-274840
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13	420.5	91.6	171	16	US-10-739-930-9314	Sequence 9314, Ap
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15	417.5	91.0	171	15	US-10-424-599-195353	Sequence 195353,
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17	417.5	91.0	178	14	US-10-180-375-197	Sequence 197, App
18	417.5	91.0	178	15	US-10-183-687-413	Sequence 413, App
19	417.5	91.0	178	15	US-10-374-780A-785	Sequence 785, App
20	417.5	91.0	178	15	US-10-399-883-32	Sequence 32, Appl
21	417.5	91.0	178	17	US-10-678-588A-3	Sequence 3, Appl1
22	417.5	91.0	178	17	US-10-675-852-46	Sequence 46, Appl
23	417.5	91.0	179	15	US-10-374-780A-786	Sequence 786, Appl
24	417.5	91.0	183	17	US-10-675-852-56	Sequence 56, Appl
25	417.5	91.0	188	17	US-10-675-852-38	Sequence 38, Appl
26	417.5	91.0	234	15	US-10-425-114-58164	Sequence 58164, A
27	414.5	90.3	141	15	US-10-112-887-2	Sequence 2, Appl1
28	414.5	90.3	141	15	US-10-225-068-114	Sequence 114, App
29	414.5	90.3	141	15	US-10-374-780A-88	Sequence 88, Appl
30	414.5	90.3	141	15	US-10-412-6998-1782	Sequence 1782, Ap
31	414.5	90.3	141	17	US-10-678-588A-7	Sequence 7, Appl1
32	414.5	90.3	141	17	US-10-675-852-2	Sequence 2, Appl1
33	414.5	90.3	141	17	US-10-225-068-114	Sequence 114, App
34	414.5	90.3	141	20	US-11-069-255-2	Sequence 20, Appl1
35	414.5	90.3	182	14	US-10-180-375-174	Sequence 174, App
36	414.5	90.3	182	15	US-10-183-687-304	Sequence 304, App
37	414.5	90.3	182	15	US-10-399-883-24	Sequence 24, Appl
38	414.5	90.1	177	14	US-10-180-375-154	Sequence 154, App
39	413.5	90.1	177	15	US-10-183-687-284	Sequence 284, App
40	413.5	90.1	177	15	US-10-399-883-4	Sequence 4, Appl1
41	413.5	90.1	215	15	US-10-374-780A-791	Sequence 791, App
42	412.5	89.9	215	15	US-10-180-375-152	Sequence 152, App
43	409.5	89.2	174	14	US-10-183-687-282	Sequence 282, App
44	409.5	89.2	174	15	US-10-183-687-282	Sequence 2, Appl1
45	409.5	89.2	174	15	US-10-399-883-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-10-678-588A-8  
Sequence 8, Application US/10678588A  
Publication No. US2005022266A1  
GENERAL INFORMATION:  
APPLICANT: Wu, Jingtui  
TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants  
FILE REFERENCE: 38-21 (52578)C  
CURRENT APPLICATION NUMBER: US/10/678,588A  
CURRENT FILING DATE: 2003-10-02  
PRIOR APPLICATION NUMBER: US 60/415,758  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: US 60/425,157  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: US 60/463,787  
PRIOR FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 8  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURES:  
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OTHER INFORMATION: Xaa can be Ala or Pro  
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OTHER INFORMATION: Xaa can be Thr or none  
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US-10-678-588a-8

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Db 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXOBCVSFISFISASXKC 60

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Db 61 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREXEG 101

RESULT 2
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; Sequence 2, Application US/10678588A
; Publication No. US20050022266A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jinghui
; TITLE OF INVENTION: Water-Deficit-TolerantTransgenic Plants
; FILE REFERENCE: 38-21(52578)C
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/ CURRENT APPLICATION NUMBER: US/10/678,588A
/ CURRENT FILING DATE: 2003-10-02
/ PRIOR APPLICATION NUMBER: US 60/415,758
/ PRIOR FILING DATE: 2002-10-02
/ PRIOR APPLICATION NUMBER: US 60/425,157
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: US 60/463,787
/ PRIOR FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 185
/ TYPE: PRT
/ ORGANISM: Zea mays
US-10-678-588a-2

Query Match      92.6%; Score 425; DB 17; Length 185;
Best Local Similarity 83.2%; Pred. No. 4.7e-50;
Matches 84; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXOBCVSFISFISASXKC 60
Db 30 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXOBCVSFISFISASXKC 89

Qy 61 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREXEG 101
Db 90 QXERKTINGDDLLMAMATLGFEDYIEPLKYLXXYREXEG 130

RESULT 3
US-10-675-852-42
; Sequence 42, Application US/10675852
; Publication No. US20050086718A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: KEDDIE, James S
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RATCHFEE, Oliver
; APPLICANT: KUMIMOTO, Roderick
; APPLICANT: GUTTERSON, Neal
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
; FILE REFERENCE: MBI-0022CIP
; CURRENT APPLICATION NUMBER: US/10/675,852
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/166,228
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/197,999
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 60/227,439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 10/112,887
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 10/286,264
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 10/225,068
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 185
```

```

; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: ZEAMA-08NOV01-CLUSTER719_3 polypeptide
US-10-675-852-42

```

```

Query Match          92.6%; Score 425; DB 17; Length 185;
Best Local Similarity 83.2%; Pred. No. 4.7e-50;
Matches 84; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

```

```

QY 1 REODRYLPINANISIRMKALPXNGKXXXXXXIAKDAKXTQECVSEFISFTSEASXKC 60
DB 30 REODRFLPINANISIRMKALPXNGKTIIPANGKTIIPANGKIADKAKETQECVSEFISFTSEASDKC 89
QY 61 QXERKRTINGDDLLMAMATIGFEDYIEPLKYYLXXYREXEG 101
DB 90 QXERKRTINGDDLLMAMATIGFEDYIEPLKYYLXXYREXEG 130

```

```

RESULT 4
US-10-374-780A-802
; Sequence 802, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2306
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 802
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Orthologous to G481, G482
; NAME/KEY: misc feature
; LOCATION: (151)..(151)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid

```

```

US-10-374-780A-802
Query Match          92.3%; Score 423.5; DB 15; Length 160;
Best Local Similarity 85.1%; Pred. No. 6.3e-50;
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

```

```

QY 1 REODRYLPINANISIRMKALPXNGKXXXXXXIAKDAKXTQECVSEFISFTSEASXKC 60
DB 27 REODRFLPINANISIRMKALPXNGK-----IAKDAKXTQECVSEFISFTSEASBKC 79
QY 61 QXERKRTINGDDLLMAMATIGFEDYIEPLKYYLXXYREXEG 101
DB 80 QXERKRTINGDDLLMAMATIGFEDYIEPLKYYLXXYREXEG 120

```

```

RESULT 5
US-10-675-852-26
; Sequence 26, Application US/10675852
; Publication No. US20050086718A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: KEDDIE, James S
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KOMIMOTO, Roderick
; APPLICANT: GUTTERSON, Neal
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
; FILE REFERENCE: MBI-0022CIP
; CURRENT APPLICATION NUMBER: US/10/675,852
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/166,228
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/197,899
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 60/227,439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 10/112,887
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 10/286,264
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (151)..(151)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: G3470 GLVMA-28NOV01-CLUSTER4778_3 polypeptide
US-10-675-852-26
Query Match          92.3%; Score 423.5; DB 17; Length 160;
Best Local Similarity 85.1%; Pred. No. 6.3e-50;
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

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QY  REODRYPLINIRIMKCALPXNGKXXXXXXXXXIAKAKTXOCVSEFISFISSEAKXC 60
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  REODRYPLINIRIMKCALPXNGK-----IAKAKTOMGCVSEFISFISSEAKXC 79
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  QXERKRTINGDILMAATGFDYDIEPLAVLYLXXYREXG 101
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  QKERRKTINGDILMAATGFDYDIEPLAVLYLXXYREXG 120
Db  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 6
US-10-424-599-274836
Sequence 274836, Application US/10424599
Publication NO. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 274836
LENGTH: 173
TYPE: PRT
ORGANISM: Glycine max
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT3847_90198C.1.pep
US-10-424-599-274836

```

	Query Match	Similarity	95.1%	Score	423.5	DB	15	Length	173
	Best Local	Similarity	92.1%	Pred. No.	6.9e-50				
	Matches	Conservative	0	Mismatches	8	Indels	7	Gaps	1
Qy	1	REQRRYLPDIANISRMKRLPANGKXXXXXXXXXADACKTQOCYSEFISPTSRASKC	60						
Db	26	REQRRYLPDIANISRMKRLPANGK-----IADACKTQOCYSEFISPTSRASKC	78						
Qy	61	QKERRKTINGDDLLAMAAATLGFEDYIEPLKVTLLXXYYREXEG	101						
Db	79	QKERRKTINGDDLLAMAAATLGFEDYIEPLKVTLLYYRREXEG	119						

```

RESULT 7
US-10-678-588A-6
Sequence 6, Application US/10678588A
Publication No. US20050022266A1
GENERAL INFORMATION:
APPLICANT: Wu, Jingrui
TITLE OF INVENTION: Water-Deficit-Tolerant Transgenic Plants
FILE REFERENCE: 38-21(52578)C
CURRENT APPLICATION NUMBER: US/10/678,588A
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,758
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/425,157
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: US 60/463,787
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
LENGTH: 173
TYPE: prt
ORGANISM: Glycine max
US-10-678-588A-6

```

Query Match	92.3%	Score 423.5	DB 17	Length 173
Best Local Similarity	85.1%	Pred. No. 6.9e-50		
Matches 86	Conservative	0	Mismatches 8	Indels 7
				Gaps 1

Qy	Db	Qy	Db
1	26	61	79
REODRTIPLANIRIMKALPKNKGGCCCCXXIXADAKTIOBCVSEFISFTTSEASXKC	REODRTIPLANIRIMKALPKNK-----IADAKTIOBCVSEFISFTTSEASXKC	QKERRKTIINDDLIMAMTIGFEDYIEPLKVIILXXRXREG	QKERRKTIINDDLIMAMTIGFEDYIEPLKVIILARIREBG
60	78	101	119

```

RESULT 8
US-10-675-852-24
; Sequence 24, Application US/10675852
; Publication No. US20050086718A1
;
GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline R
; APPLICANT: KENDRICK, James S
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEIDA, Omaira
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RAYCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick
; APPLICANT: GUTTERSON, Neal
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
; FILE REFERENCE: MBI-0022CIP
; CURRENT APPLICATION NUMBER: US/10/675,852
; CURRENT FILING DATE: 2003-09-30
;
PRIOR APPLICATION NUMBER: 10/412,659
; PRIOR FILING DATE: 2003-04-10
;
PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
;
PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
;
PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
;
PRIOR APPLICATION NUMBER: 60/166,228
; PRIOR FILING DATE: 1999-11-17
;
PRIOR APPLICATION NUMBER: 60/197,899
; PRIOR FILING DATE: 2000-04-17
;
PRIOR APPLICATION NUMBER: 60/227,439
; PRIOR FILING DATE: 2000-08-22
;
PRIOR APPLICATION NUMBER: 10/112,887
; PRIOR FILING DATE: 2002-03-18
;
PRIOR APPLICATION NUMBER: 10/286,264
; PRIOR FILING DATE: 2003-01-23
;
PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
;
Remaining prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 104
;
SOFTWARE: PatentIn version 3.2
;
SEQ ID NO 24
;
LENGTH: 173
;
TYPE: PRT
;
ORGANISM: Glycine max
;
FEATURE:
;
OTHER INFORMATION: G3471 GLYMA-28N0V01-CLUSTER4778_1 polypeptide
US-10-675-852-24

```

Query Match	Similarity	Score	423.5	DB	17	Length	173
Best Local	85.1%	Pred.	6.9e-50				
Matches	86	Conservative	0	Mismatches	8	Indels	7
						Gaps	1

  

Qy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60															
Db	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

QY 61 QEKRKTINGDDLLMAMATLGFEDYIEPLKVLYLXXYREXEG 101  
Db 79 QEKRKTINGDDLLMAMATLGFEDYIEPLKVLYLARYREAEG 119

## RESULT 9

US-10-424-599-274840  
 ; Sequence 274840, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 274840  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_90200C.1.pep  
 US-10-424-599-274840

Query Match 92.3%; Score 423.5; DB 15; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 7e-50;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQBCVSEFISFISEASKC 60  
 DB 27 REODRYLPINISIRIMKALPXNGK-----IAKDAKDTMQBCVSEFISFISEASKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVVYLXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFEDYIEPLKVVYLARREAG 120

RESULT 10  
 US-10-425-114-39733  
 ; Sequence 39733, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaka, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 39733  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700677948\_FLI.pep  
 US-10-425-114-39733

Query Match 92.3%; Score 423.5; DB 15; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 7e-50;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQBCVSEFISFISEASKC 60  
 DB 27 REODRYLPINISIRIMKALPXNGK-----IAKDAKDTMQBCVSEFISFISEASKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVVYLXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFEDYIEPLKVVYLARREAG 120

RESULT 11  
 US-10-675-852-84  
 ; Sequence 84, Application US/10675852  
 ; Publication No. US20050086718A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mendel Biotechnology, Inc.  
 ; APPLICANT: Heard, Jacqueline E  
 ; APPLICANT: KEDDIE, James S  
 ; APPLICANT: CREELMAN, Robert A  
 ; APPLICANT: PINEDA, Omar A  
 ; APPLICANT: JIANG, Cai-Zhong  
 ; APPLICANT: RATCHLIFE, Oliver  
 ; APPLICANT: KUMIMOTO, Roderick  
 ; APPLICANT: GUTTERSON, Neal  
 ; APPLICANT: SHERMAN, Bradley K  
 ; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS  
 ; FILE REFERENCE: MBI-0022CIP  
 ; CURRENT APPLICATION NUMBER: US/10/675,852  
 ; CURRENT FILING DATE: 2003-09-30  
 ; PRIOR APPLICATION NUMBER: 10/412,699  
 ; PRIOR FILING DATE: 2003-04-10  
 ; PRIOR APPLICATION NUMBER: 09/533,030  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: 60/125,814  
 ; PRIOR FILING DATE: 1999-03-23  
 ; PRIOR APPLICATION NUMBER: 09/713,994  
 ; PRIOR FILING DATE: 2000-11-16  
 ; PRIOR APPLICATION NUMBER: 60/166,228  
 ; PRIOR FILING DATE: 1999-11-17  
 ; PRIOR APPLICATION NUMBER: 60/197,899  
 ; PRIOR FILING DATE: 2000-04-17  
 ; PRIOR APPLICATION NUMBER: 60/227,439  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 10/112,887  
 ; PRIOR FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 10/286,264  
 ; PRIOR FILING DATE: 2003-01-23  
 ; PRIOR APPLICATION NUMBER: 10/225,068  
 ; PRIOR FILING DATE: 2002-08-09  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 84  
 ; LENGTH: 174  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: G3477 polypeptide  
 US-10-675-852-84

Query Match 92.3%; Score 423.5; DB 17; Length 174;  
 Best Local Similarity 85.1%; Pred. No. 7e-50;  
 Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;  
 QY 1 REODRYLPINISIRIMKALPXNGKXXXXXXIAKDAKXTXQBCVSEFISFISEASKC 60  
 DB 27 REODRYLPINISIRIMKALPXNGK-----IAKDAKDTMQBCVSEFISFISEASKC 79  
 QY 61 QXERKRTINGDDLLMAMATLGFEDYIEPLKVVYLXXYREXEG 101  
 DB 80 QXERKRTINGDDLLMAMATLGFEDYIEPLKVVYLARREAG 120

RESULT 12  
 US-10-425-114-48992  
 ; Sequence 48992, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jindong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaka, Jack E

```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48992
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700554268_FLI.pep
US-10-425-114-48992

Query Match          92.3%; Score 423.5; DB 15; Length 185;
Best Local Similarity 85.1%; Pred. No. 7.5e-50;
Matches 86; Conservative 0; Mismatches 8; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIXAKDAKXTXQBCVSEFISFITSASXKC 60
    |||||
Db 38 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQBCVSEFISFITSASXKC 90
    |||||

Qy 61 QXERKKTINGDDLLMAMATGFEFDYIEPLKYYLXXYREXEG 101
    |||||
Db 91 QXERKKTINGDDLLMAMATGFEFDYIEPLKYYLXXYREXEG 131
    |||||

RESULT 13
US-10-739-930-9314
; Sequence 9314, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kowalig, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(5317)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 9314
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GUYMA-23APR03-C6781_1.p
US-10-739-930-9314

Query Match          91.6%; Score 420.5; DB 16; Length 171;
Best Local Similarity 83.2%; Pred. No. 1.8e-49;
Matches 84; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIXAKDAKXTXQBCVSEFISFITSASXKC 60
    |||||
Db 25 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQBCVSEFISFITSASXKC 77
    |||||

Qy 61 QXERKKTINGDDLLMAMATGFEFDYIEPLKYYLXXYREXEG 101
    |||||
Db 78 QXERKKTINGDDLLMAMATGFEFDYIEPLKYYLXXYREXEG 118
    |||||

RESULT 14
US-10-675-852-64
; Sequence 64, Application US/10675852
; Publication No. US20050086718A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline B
; APPLICANT: KEDDIE, James S
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaria
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: RATCLIFFE, Oliver
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; APPLICANT: KUMIMOTO, Roderick
; APPLICANT: GUTTERSON, Neal
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
; FILE REFERENCE: MBI-0022CIP
; CURRENT APPLICATION NUMBER: US/10/675,852
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/166,228
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/197,899
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 60/227,439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 10/112,887
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 10/286,264
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; OTHER INFORMATION: SGN-UNIGENE-46859 polypeptide
US-10-675-852-64

Query Match          91.6%; Score 420.5; DB 17; Length 176;
Best Local Similarity 84.2%; Pred. No. 1.8e-49;
Matches 85; Conservative 1; Mismatches 8; Indels 7; Gaps 1;

Qy 1 REODRYLPINISIRIMKALPXNGKXXXXXXIXAKDAKXTXQBCVSEFISFITSASXKC 60
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Db 33 REODRYLPINISIRIMKALPXNGK-----IAKDAKXTXQBCVSEFISFITSASXKC 85
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Qy 61 QXERKKTINGDDLLMAMATGFEFDYIEPLKYYLXXYREXEG 101
    |||||
Db 86 QXERKKTINGDDLLMAMATGFEFDYIEPLKYYLXXYREXEG 126
    |||||

RESULT 15
US-10-424-599-195353
; Sequence 195353, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalig David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195353
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18430C.1.ppe
US-10-424-599-195353
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